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(54) **EDIBLE CELL BASED VACCINES**

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(57) **ABSTRACT**
The present invention provides animal cells that have been engineered to express one or more viral antigens. The engineered cells can be formulated into cultured meat products that can be used as edible vaccines.
Specification includes a Sequence Listing.

EDIBLE CELL BASED VACCINES**CROSS-REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims benefit to U.S. Provisional Application No. 63/043,635 filed on Jun. 24, 2020, the contents of which are incorporated by reference in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under grant P41EB027062 awarded by the National Institutes of Health. The government has certain rights in the invention.

SEQUENCE LISTING

[0003] A Sequence Listing accompanies this application and is submitted as an ASCII text file of the sequence listing named "166118_01054_ST25.txt" which is 216 KB in size and was created on Jun. 10, 2021. The sequence listing is electronically submitted via EFS-Web with the application and is incorporated herein by reference in its entirety.

BACKGROUND

[0004] Vaccination is the preferred mode of preventing infectious disease. Safe and effective vaccines have been employed for over 60 years and have reduced the number of deaths caused by infectious diseases by more than 95% (Bonanni et al., 2015). Despite this success, infectious diseases remain a leading cause of death globally. Researchers estimate that 20% of infectious disease-related deaths could be prevented by currently available vaccines (World Health Organization, 2015). For example, the global mortality rate for the flu is between 290K and 650K deaths per year. Yet, despite the widespread availability of the flu vaccine in the United States, the 2017-2018 flu season resulted in up to 45 million illnesses, 810 million hospitalizations, and 61,000 deaths (Centers for Disease Control and Prevention, 2020). A significant portion of these cases are thought to be due to the limited number of people who receive seasonal flu vaccinations. For instance, for the 2018-2019 flu season, 41% of Americans reported they did not intend to get a flu vaccine.

[0005] Current vaccine production techniques are plagued by numerous limitations, including lengthy production times, distribution limits, and suboptimal routes of administration. For example, each year, it takes approximately 7 months to develop egg-based and cell-based seasonal influenza vaccines and approximately 5 months to develop recombinant-based vaccines (Chen et al., 2020). Further, the ideal storage temperature for conventional influenza vaccines is 5° C. and temperature fluctuations can reduce antigen efficacy. Thus, to reduce the immunization coverage gap in developing countries, the range of allowable temperatures for vaccine storage and distribution must be widened (Ashok et al., 2017). Finally, the seasonal influenza vaccine is predominantly administered via an intramuscular injection, despite the fact that many Americans (28%) avoid receiving a flu shot due to a fear of needles (Young, 2018). Furthermore, oral or nasal administration is superior to

intramuscular administration because it stimulates both mucosal (i.e., IgA antibodies) and systemic (i.e., IgG antibodies) immunity.

[0006] When oral administration of vaccines is possible, it is often preferred due to improved safety and convenience. However, patient compliance can also be an issue for conventional oral administration of drugs, as 10-20% of the population reports difficulty swallowing pills (Schiele et al., 2013). Thus, there is growing interest in edible vaccines, i.e., vaccines that are provided as a food formulation. To date, edible vaccines have been explored primarily in the form of plant-based vaccines, in which consumable plants are engineered to produce antigens against infectious agents. The benefits of edible vaccines include less stringent storage requirements, increased patient compliance, and reduced production, administration, and distribution costs. Further, edible vaccines have reduced side effects due to lack of pathogens, toxins, and allergens (e.g., from eggs) that are commonly present in traditional vaccines. While their benefits are noteworthy, edible plant-based vaccines have several limitations, including variability in antigen concentration, differences in plant versus human glycosylation patterns, and a lack of comprehensive research.

[0007] Thus, there is a need in the art for improved oral vaccination platforms and edible vaccines.

SUMMARY OF THE INVENTION

[0008] In a first aspect, the present invention provides an engineered cell comprising a heterologous polynucleotide encoding a viral antigen. The cell may be a muscle cell, a muscle precursor cell, a fibroblast, or an adipocyte from a non-human mammal, an insect, or a fish.

[0009] In a second aspect, the present invention provides a cultured meat product comprising comprising an engineered cell described herein seeded on a food safe substrate. In some aspects, the meat product comprises a confluent serum-free culture of the engineered cells.

[0010] In a third aspect, the present invention provides an edible vaccine comprising a cultured meat product described herein or an engineered cell described herein.

[0011] In a fourth aspect, the present invention provides a method for inducing an immune response against a virus in a subject. The method comprises administering an effective amount of an edible vaccine described herein to the subject.

DETAILED DESCRIPTION OF THE INVENTION

[0012] The present invention provides cells that have been engineered to express one or more viral antigens. The engineered cells can be formulated into cultured meat products that can be used as edible vaccines.

[0013] Recent advances in in vitro meat production provide an opportunity to develop new edible vaccine formulations, in which antigens are expressed in cells that are combined to form a cultured meat product. These cultured meat-based edible vaccines may offer advantages over plant-based edible vaccines in terms of improved dose control and consistency, improved bioavailability and drug activity, improved glycosylation patterns, and reduced susceptibility to natural factors. Importantly, cultured meat-based edible vaccines also offer several significant advantages over conventional vaccines. For example, edible vaccines (1) can be produced rapidly, i.e., in 3-4 months as compared to the 7

months required to produce egg-based and cell-based vaccines; (2) have a widened range of allowable storage temperatures due to the stabilization of antigens within cells/tissues up until the point of delivery; (3) stimulate both mucosal and systemic immunity; and (4) circumvent issues with patient needle/pill compliance.

Engineered Cells:

[0014] In a first aspect, the present invention provides an engineered cell comprising a heterologous polynucleotide encoding a viral antigen. The cell may be a muscle cell, a muscle precursor cell, a fibroblast, or an adipocyte from a non-human mammal, an insect, a fish, or a bird.

[0015] As used herein, the term “engineered cell” refers to a cell that comprises an exogenous polynucleotide. The cells of the present invention may be generated by introducing one or more heterologous polynucleotides encoding a viral antigen into the cell to produce a genetically engineered cell. The cell may be engineered to transiently or stably express the viral antigen. The heterologous polynucleotide encoding the viral antigen may be introduced into the cell using any transfection, transformation, or transduction method known in the art (e.g., via microinjection, encapsulation, or electroporation). In some embodiments, the polynucleotide is integrated into the genome of the cell. For example, the polynucleotide may be integrated into the genome using a zinc-finger nuclease, TALENs, CRISPR/Cas mediated genome editing, or a transposon (e.g., Sleeping Beauty, PiggyBac, Tol1, Tol2, Minos, Frog Prince, Passport, Hsmar1, or Harbinger3_DR). Other suitable methods may be used that are well known and understood in the art.

[0016] As used herein, the terms “polynucleotide” and “nucleic acid” are used interchangeably to refer to a polymer of DNA or RNA, which may be of natural or synthetic origin. The polynucleotides of the present invention are “heterologous”, meaning they are not naturally associated with the host cell into which they have been introduced.

[0017] The polynucleotides may be provided to the cell in the form of a construct or a vector (i.e., a construct or vector comprising a polynucleotide described herein). As used herein, the term “construct” refers to an artificially constructed polynucleotide. Constructs may be entirely synthetic or may be recombinant polynucleotides that comprise polynucleotide sequences derived from at least two different natural sources. The term “vector” refers to a nucleic acid molecule that is capable of propagating another nucleic acid to which it is linked. The term includes the vector as a self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. Vectors suitable for use with the present invention comprise a polynucleotide encoding a viral antigen described herein and additional heterogeneous sequence necessary for proper propagation of the vector and expression of the encoded antigen. Suitable vectors include, for example, episomal vectors, viral vectors (e.g., retrovirus, adenovirus, baculovirus), plasmids, and RNA vectors.

[0018] The construct or vector used with the present invention may include a promoter that is operably linked to one or more polynucleotides described herein. As used herein, the term “promoter” refers to a DNA sequence capable of controlling the expression of a downstream coding sequence. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even

comprise synthetic DNA segments. The promoter used with the present invention may be a heterologous promoter (i.e., a promoter that is not naturally associated with the host cell genome) or an endogenous promoter. Suitable promoters for use with the present invention include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, chemically regulated, tissue-preferred, and tissue-specific promoters. The promoter may be a plant, animal, bacterial, fungal, or synthetic promoter. Promoters that are commonly used in mammalian cells include, without limitation, promoters for Rous sarcoma virus (RSV), human immunodeficiency virus (HIV-1), cytomegalovirus (CMV), Dox-inducible promoter (e.g., Tet Response Element (TRE)), ubiquitin C (Ubc), CMV early enhancer/chicken beta actin (CAG), human beta actin, phosphoglycerate kinase 1 (PGK1), SV40 virus, and the like. Promoters that are commonly used in insect cells include upstream activating sequence (UAS), actin 5c (Ac5), and polyhedrin. Promoters that are commonly used in fish cells include *Xenopus laevis* elongation factor 1 α promoter (XIEef1a1) and ocean pout antifreeze protein promoter (OP5a). Other suitable promoters include the T3, T7 and SP6 promoter sequences, which are often used for in vitro transcription of RNA.

[0019] In some embodiments, the construct or vector used with the present invention encodes a reporter protein. A “reporter protein” is a protein that confers to a cell a characteristic that is easily identified or measured. A reporter protein is often used to indicate whether a certain gene has been taken up by or expressed in the cell. Suitable reporter proteins include, for example, proteins that can produce a fluorescent signal, luminescent signal, colorimetric signal, wavelength absorbance, or radioactive signal. Exemplary reporter proteins include β -glucuronidase (GUS), β -lactamase, luciferase, α -amylase, green fluorescence protein, and α -galactosidase, among others. In some embodiments, the reporter protein is a selectable marker. As used herein, the term “selectable marker” refers to a protein that protects a cell from a selection agent that would normally kill it or prevent its growth or a protein that allows for identification of the cell in which it is produced. A selectable marker may be a compound that confers resistance to an otherwise toxic compound. For example, in some embodiments, the selectable marker confers resistance to an antibiotic. Cells that have been transfected with a construct encoding a selectable marker can be exposed to the selection agent to select for cells comprising the construct. In another embodiment, the selectable marker may be a fluorescent protein.

[0020] As used herein, the term “antigen” refers to a molecule that can initiate an immune response (i.e., a humoral and/or a cellular immune response) in a recipient. Antigens can be any type of biologic molecule including, for example, simple intermediary metabolites, sugars, lipids, and hormones as well as macromolecules such as complex carbohydrates, phospholipids, nucleic acids, and proteins. The antigens used with the present invention are “viral antigens”, meaning that they are virus-specific antigens that elicit an immune response against a virus in a recipient. Typically, a viral antigen is present on the surface of the virus and triggers an immune response in the recipient by reacting with or binding to one or more immune cells.

[0021] The viral antigen used with the present invention may be from any virus of interest. For example, in some embodiments, the viral antigen is from an influenza, a

coronavirus, hepatitis B, a human papilloma virus, a parvovirus, or a Norwalk virus, among others. Suitable antigens derived these viruses include, for example, an influenza hemagglutinin protein, an influenza neuraminidase protein, an influenza matrix protein, a coronavirus spike protein, a coronavirus envelope protein, a coronavirus membrane protein, a coronavirus receptor binding domain protein, a major hepatitis B surface antigen protein, a human papillomavirus L1 protein, a parvovirus viral protein, and a Norwalk virus capsid protein. A more detailed description of these viral antigens is provided in Example 2, and exemplary amino acid sequences of these antigens are provided as SEQ ID NOs:1-50. The polynucleotides of the present invention may encode one or more of these exemplary antigens or an immunogenic fragment thereof.

[0022] Influenza vaccines are commonly formulated against multiple influenza subtypes. For example, three influenza subtypes (i.e., H₁N₁, H₃N₂, or H₅N₁) are combined to create a trivalent influenza vaccine. Thus, in some embodiments, the cell is engineered to express a combination of HA proteins from the H₁N₁, H₃N₂, and H₅N₁ influenza subtypes. In some embodiments, the viral antigen has a sequence that is at least 85%, 90%, 95%, 98%, 99%, or 99.9% identical to SEQ ID NO:1 (i.e., HA type 1), SEQ ID NO:3 (i.e., HA type 3), and/or SEQ ID NO:5 (i.e., HA type 5).

[0023] “Percentage of sequence similarity” or “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Protein and nucleic acid sequence identities are evaluated using the Basic Local Alignment Search Tool (“BLAST”), which is well known in the art (Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87: 2267-2268; Altschul et al., 1997, *Nucl. Acids Res.* 25: 3389-3402). The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as “high-scoring segment pairs,” between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula (Karlin and Altschul, 1990), the disclosure of which is incorporated by reference in its entirety. The BLAST programs can be used with the default parameters or with modified parameters provided by the user.

[0024] In some embodiments, the cell is engineered to express a virus-like particle (VLP). As used herein, a “virus-like particle (VLP)” is a particle that includes one or more viral proteins and mimics at least a portion of the structure of the native virus but lacks the viral genome. The VLP may include any combination of the viral antigen proteins as described herein. In some embodiments, the VLP includes at least one influenza HA protein. In some embodiments, the

VLP includes at least two influenza HA proteins. In some embodiments, the VLP includes at least three influenza HA proteins. Preferably, the one or more HA proteins are for variant strains of influenza, and thus will confer an immune response to multiple strains of influenza within one VLP.

[0025] In some embodiments, the cell is engineered to express the viral antigen as a fusion protein with a protein adjuvant. As used herein, the term “adjuvant” refers to a substance that enhances the body’s immune response to an antigen. Suitable protein adjuvants may include, but are not limited to, interleukin 12 (IL-12), cucumber mosaic virus tetanus toxoid (CMV-TT), and bacterial toxins (Cholera toxin, heat labile enterotoxin), among others. One skilled in the art is able to determine suitable protein adjuvants for use in the present invention.

[0026] The engineered cell of the present invention may be any animal cell that can be stably maintained, grown, and expanded in culture. Suitable animal cells for use with the present invention include, mammalian cells, insect cells, fish cells, and avian cells. Suitable mammalian cells include porcine, bovine, cervine, hircine, leporine, and murine cells. In some embodiments, the cell is from a cow of the species *Bos taurus*. For use in a cultured meat product, as described below, the mammalian cell is a non-human mammalian cell.

[0027] Methods for use of genetically engineered cells in a cultured meat product are described, for example, in Publication No. WO2020243695 of International Application No. PCT/US2020/035526, which is incorporated herein by reference in its entirety. Methods for the use of insect cells, specifically, in a cultured meat product are described in Publication No. WO2020131661 of International Application No. PCT/US2019/066452, which is incorporated herein by reference in its entirety. The present engineered cell in the cultured meat product designed herein may as described in either of these publications.

[0028] The animal cells of the present invention may be any type of cell including, for example, a primary cell, an immortalized cell, or a cell differentiated from a pluripotent cell (e.g., an embryonic stem cell, induced pluripotent cell, etc.). Primary cells may be grown and proliferated in culture for 1, 2, 3, 4, 5, 6, or more passages prior to use. In some embodiments, the cell is an immortalized cell that expresses TERT and CDK4 and has been spontaneously immortalized through continuous culture, or engineered to express other immortalization genes.

[0029] In some embodiments, the cell is a mammalian cell. In some embodiments, the mammalian cell is muscle precursor cell. For example, in some embodiments, the cell is a mammalian muscle precursor cell that expresses paired box protein 7 (Pax7). In some embodiments, the cell is a muscle precursor satellite cell that expresses Pax7. In some embodiments, the cell is a Pax7+ bovine satellite cell.

[0030] In other embodiments, the mammalian cell is a muscle cell. Mammalian muscle cells can be characterized by the expression of actin, myogenin, and myosin heavy chain (MHC) and the formation of multinucleated myotubes. For example, in some embodiments, the cell is a MHC⁺ actin⁺ mammalian multinucleated myotube. In some embodiments, the myotube is produced by differentiation from mammalian satellite cells. To differentiate the satellite cells into myotube cells, the satellite cells are cultured to confluency in any culture medium that supports their growth (e.g., B8 medium or DMEM+20% fetal bovine serum). Then, the confluent cells are differentiated in culture

medium that includes a Neurobasal/L15 (1:1) basal media supplemented with epidermal growth factor (EGF; 0.01-5 ng/ml; preferably 0.5 ng/mL), insulin-like growth factor 1 (IGF-1; 0.01-5 ng/ml; preferably 0.05 ng/mL), and 1% Antibiotic-Antimycotic. In some embodiments, the cells are differentiated for 3-30 days.

[0031] In other embodiments, the mammalian cell is an adipocyte. Mammalian adipose cells are characterized by expression of peroxisome proliferator-activated receptor gamma (PPAR γ) and increased lipid production. In some embodiments, the adipocyte is produced by differentiation from mammalian satellite cells. Lipid accumulation can be initiated in satellite cells using a differentiation media containing free fatty acids (FFAs). Specifically, a 3-FFA cocktail of linoleic acid, erucic acid, and elaidic acid at equal concentrations (e.g., between about 10 μ M and about 500 μ M) induces accumulation of intracellular lipids over about six days in culture. A more detailed description of adipogenic differentiation from mammalian satellite cell is provided in Fish et al. (Trends Food Sci Technol., 2020, 98:53-67), which is incorporated by reference herein.

[0032] In other embodiments, the cell is an insect cell. In some embodiments, the insect cell is a muscle cell or a muscle precursor cell (i.e., a muscle progenitor-like cell). Insect muscle cells are long, multinucleated myotubes that can be identified by expression of myosin heavy chain and ecdysone receptor (EcdR). In some embodiments, insect muscle cells also express connectin and/or neuroglian. Insect muscle cells can also be characterized by spontaneous cell contraction or by contraction following stimulation with extracellular potassium. Additionally, insect muscle cells can be characterized by growth and survival in the prolonged absence of medium refreshment. For example, the insect muscle cells can survive and grow for at least about 2 days, at least about 5 days, at least about 10 days, at least about 15 days, at least about 20 days, or at least about 25 days when the medium is not changed or supplemented. In some embodiments, the insect muscle cells are primary *Drosophila* muscle cells. In some embodiments, the insect muscle cells are primary cells from *Manduca sexta* embryos or adult muscles. In some embodiments, the insect muscle cells are derived from *Manduca sexta* embryonic precursor cells (Ms-EPC). In some embodiments, the insect muscle precursor cells are *Drosophila melanogaster* adult muscle progenitor-like cells (DrAMPCs).

[0033] In some embodiments, the insect muscle cell is produced by differentiation of an insect muscle progenitor-like cell. This is accomplished by culturing the insect muscle progenitor-like cells in serum-free culture medium including insect molting hormone 20-hydroxyecdysone (20-HE) for a time under suitable conditions for cells to elongate and fuse (i.e., differentiate). In some embodiments, the insect muscle progenitor-like cells are cultured while adhered to a substrate in serum-free culture medium including 20-HE. Insect muscle progenitor-like cell are cultured in serum-free culture medium supplemented with 20-HE for at least about 0.5 days, at least about 1 day, at least about 2 days, at least about 3 days, or at least about 5 days to form insect muscle cells expressing myosin heavy chain and EcdR. In some embodiments, differentiation of insect muscle cells is observed after about 24 hours in culture with 20-HE. 20-HE is present in the culture medium at a concentration of at least 20 ng/ml, at least about 30 ng/ml, at least about 40 ng/ml, at least about 50 ng/ml, at least about 75 ng/ml, at least about 100 ng/ml,

at least about 200 ng/ml, at least about 300 ng/ml, at least about 400 ng/ml, at least about 500 ng/ml, at least about 600 ng/ml, at least about 700 ng/ml, at least about 800 ng/ml, at least about 900 ng/ml, or at least about 100 ng/ml. The 20-HE may be present in the culture medium at a concentration of between about 20 ng/ml and about 2000 ng/ml, between about 40 ng/ml and about 1500 ng/ml, between about 50 ng/ml and about 1000 ng/ml, between about 100 ng/ml and about 1000 ng/ml, or between about 100 ng/ml and about 500 ng/ml. In some embodiments, the serum-free culture medium is a commercially available culture medium such as Ex-Cell 405. In some embodiments, the insect muscle progenitor-like cells are adhered to a substrate in the presence of serum-free culture medium then supplemented with 20-HE. In some embodiments, the insect muscle progenitor-like cells are cultured in serum-free medium supplemented with 20-HE while adhered to a substrate coated with Concanavalin A, laminin, and/or poly-lysine. In some embodiments, the culture additionally includes methoprene (JH). In some embodiments, the culture additionally includes sericin protein. In some embodiments, the culture additionally comprises an anti-agglomeration agent, such as dextran sulfate.

Cultured Meat:

[0034] In a second aspect, the present invention provides a cultured meat product comprising a confluent, serum-free culture comprising an engineered cell described herein seeded on a food safe substrate.

[0035] As used herein, a “cultured meat product” is an edible meat product produced from cell culture rather than a whole organism. Ideally, a cultured meat product is visually identical to farmed meat and is palatable to consumers. Methods for producing cultured meat are known and described in the art. See, for example, Post (Meat Science, 2012, 92, 297-301), Warner (Animal, 2019, 13(12):3041-3058), U.S. Pat. Nos. 6,835,390, and 7,270,829.

[0036] The cultured meat products of the present invention include engineered cells described herein seeded on a food safe substrate and cultured to confluence. As used herein, “confluent” refers to cells in tissue culture that form a cohesive single cell layer that covers the substrate. The cells are seeded on the substrate at a density between about 20,000 cell/cm² and about 400,000 cell/cm², between about 30,000 cells/cm² and about 350,000 cells/cm², or between about 35,000 cells/cm² and about 300,000 cells/cm². In some embodiments, the cells are seeded at a density of about 50,000 cells/cm². In some embodiments, the cells are seeded at a density of about 40,000 cells/cm², about 50,000 cells/cm², about 60,000 cells/cm², about 70,000 cells/cm², about 80,000 cells/cm², about 100,000 cells/cm², about 150,000 cells/cm², about 200,000 cells/cm², about 250,000 cells/cm², about 300,000 cells/cm² or about 350,000 cells/cm². In some embodiments, the cells become non-adherent on the food safe substrate once they reach confluence and lift off the food safe substrate without enzymatic dissociation.

[0037] In addition to the engineered cells described herein, the cultured meat products may include the plant based proteins and unmodified (i.e., wild-type) plant or animal cells. In some embodiments, the engineered cells described herein make up about 1% to about 100% of the cultured meat product based on weight or based on cell count.

[0038] As used herein, “serum-free” refers to culture conditions that do not contain serum or serum replacement, or

that contain essentially no serum or serum replacement. For example, an essentially serum-free medium can contain less than about 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% serum. As used herein, “serum-replacement,” refers to an animal serum or animal product-based replacements for the serum traditionally used in culture medium.

[0039] In some embodiments, the culture medium may include a plant-based or yeast-based extract in place of serum. Exemplary yeast and plant-based serum alternatives include hydrolyzed proteins from soy, yeast, wheat gluten, cottonseed, or corn, as well as rapeseed peptide fractions, maitake mushroom extract, and silk derived sericin protein. Plant-based and yeast-based serum alternatives do not fall under the definition of “serum-replacement”. In other words, a culture medium that comprises a plant-based or yeast-based serum alternative can be considered serum-free.

[0040] One example of a serum-free medium that can be used with the present invention is B8. B8 medium includes DMEM:F12 (1:1) basal medium supplemented with L-ascorbic acid 2-phosphate (0.1 ug/ml to 500 ug/ml; preferably about 200 ug/mL), insulin (0.1 ug/ml to 100 up/ml; preferably about 20 ug/mL), transferrin (0.1 ug/ml to 100 ug/ml; preferably about 20 ug/mL), sodium selenite (0.1 ug/ml to 100 ug/ml; preferably 20 ng/mL), FGF-2 (0.01 ug/ml to 100 ug/ml; preferably 10 ng/mL), neuregulin 1 (NRG-1; 0.001 ng/ml to 50 ng/ml; preferably 0.1 ng/mL), and TGFβ-3 (0.001 ng/ml to 50 ng/ml; preferably 0.1 ng/uL). In some embodiments, B8 medium additionally includes insulin-like growth factor 1 (IGF-1; about 10 ng/mL).

[0041] In some embodiments, the medium used in the cultured meat product is a defined medium. The terms “defined culture medium” and “defined medium” indicate that the identity and quantity of each medium ingredient is known.

[0042] In some embodiments, the culture medium includes, cinnamon, monolaurin (a derivative of coconut lauric acid), honey, or combinations thereof in addition to or instead of an antibiotic component.

[0043] Culturing can take place in any appropriate vessel (e.g., in two-dimensional plates or three-dimensional shaker flask culture). In some embodiments, the cells are cultured in shaker flasks. In some embodiments, the cells are cultured in a static suspension culture (e.g., in ultra-low attachment plates).

[0044] To form the cultured meat products of the present invention, engineered cells are seeded on a food safe substrate. As used herein, the term “food safe substrate” refers to substrates that are edible or are safe for human consumption. Such substrates are necessary in case a portion of the substrate remains affixed to the cultured meat product when it is consumed. Suitable food safe substrates are known in the art and include, but are not limited to, chitosan substrates, cellulosic substrates, silk substrates, alginate substrates, starch substrates, textured vegetable protein substrate, mycelium substrates, and whey substrates.

[0045] In some embodiments, the substrate is a chitosan substrate. Chitosan may be derived from the chitin of organisms including, but not limited to, mushrooms, crustaceans, insects, green algae, and yeast. In some embodiments, the food safe substrate is a mushroom-chitosan substrate. The chitosan substrate can be tuned to change the adherence and growth of the mammalian muscle cell culture. For example, increasing the chitosan concentration in the

substrate generally decreases adhesion of the mammalian muscle cells. The concentration of chitosan in the food safe substrate of the cultured meat product can be 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 12%, or 14%. In some embodiments, the concentration of chitosan is between about 1% and about 8%. In some embodiments, the concentration of chitosan is between about 2% and about 6%. In some embodiments, the concentration of chitosan is at least about 1%, at least about 2%, at least about 3%, at least about 4%, at least about 5%, at least about 6%, at least about 7%, or at least about 8%.

[0046] In other embodiments, the food safe substrate is a cellulose-based substrate, such as a substrate formed from decellularized plants (e.g., decellularized spinach or apples).

[0047] In some embodiments, the food safe substrate is in the form of a two-dimensional film. In other embodiments, the food safe substrate is in the form of a three-dimensional matrix or sponge, and the mammalian muscle cells form continuous muscle fibers when cultured in the matrix or sponge substrate.

[0048] Three-dimensional chitosan substrates or sponges suitable for use in the formation of muscle fibers and cultured meat products described herein can be produced using methods known in the art. For example, chitosan sponges can be formed using directional freezing. In this method, chitosan is dissolved in a solvent (e.g., acetic acid) and the chitosan solution is poured into tubes. One end of the tubes is exposed to a freezing agent (e.g., liquid nitrogen or a slurry of dry ice and ethanol) until the entire solution is frozen. The frozen chitosan is then lyophilized to form the chitosan sponge. The mechanical properties of the chitosan sponge can be tuned by altering the chitosan concentration. Sponges formed using a low concentration chitosan solution (e.g., 1%, 2%, 3% chitosan) have a lower elastic moduli, whereas sponges formed using a high concentration chitosan solution (e.g., 6%, 7%, 8% chitosan) have higher elastic moduli.

Edible Vaccines:

[0049] In a third aspect, the present invention provides an edible vaccine comprising a cultured meat product described herein or an engineered cell described herein.

[0050] As used herein, the term “vaccine” refers to a composition containing an antigen. A vaccine is administered to an individual to stimulate that individual’s immune response to said antigen. The vaccines of the present invention are “edible”, meaning that they are safe to eat.

Methods:

[0051] In a fourth aspect, the present invention provides a method for inducing an immune response against a virus in a subject. The method comprises administering an effective amount of an edible vaccine described herein to the subject.

[0052] As used herein, the term “administering” refers to any method of providing a pharmaceutical preparation to a subject. Common methods of administering a vaccine include oral administration, subcutaneous administration, intramuscular administration, intradermal administration, and intranasal administration. In preferred embodiments, the edible vaccine is administered orally. The edible vaccines may be administered in a prophylactic manner (i.e., to prevent or ameliorate the effects of a future viral infection) or in a therapeutic manner (i.e., to treat a viral infection).

[0053] The terms “effective amount” or “therapeutically effective amount” refer to an amount of a vaccine that is sufficient to induce an immune response in a subject that has received the vaccine. Ideally, the effective amount is sufficient to prevent signs or symptoms of infection by the target virus. Humoral immunity, cell mediated immunity, or both humoral and cell mediated immunity may be induced. The immunogenic response of an animal to a vaccine may be evaluated indirectly, e.g., through measurement of antibody titers or lymphocyte proliferation assays, or directly, e.g., by monitoring signs and symptoms after challenge with the target virus. The protective immunity conferred by a vaccine may be evaluated by measuring a reduction in clinical signs, e.g., the mortality, morbidity, temperature, physical condition, or overall health of the subject. The amount of a vaccine that is therapeutically effective may vary depending on the particular preparation used and the condition of the subject, and may be determined by a physician.

[0054] The “subject” to which the methods are applied may be a mammal or a non-mammalian animal, such as a bird. Suitable mammals include, but are not limited to, humans, cows, horses, sheep, pigs, goats, rabbits, dogs, cats, bats, mice and rats. In certain embodiments, the methods may be performed on lab animals (e.g., mice and rats) for research purposes. In other embodiments, the methods are used to treat commercially important farm animals (e.g., cows, horses, pigs, rabbits, goats, sheep, and chickens) or companion animals (e.g., cats and dogs). In a preferred embodiment, the subject is a human.

[0055] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. All definitions, as defined and used herein, should be understood to control over dictionary definitions, definitions in documents incorporated by reference, and/or ordinary meanings of the defined terms.

[0056] All references, patents and patent applications disclosed herein are incorporated by reference with respect to the subject matter for which each is cited, which in some cases may encompass the entirety of the document.

[0057] The indefinite articles “a” and “an,” as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean “at least one.”

[0058] The phrase “and/or,” as used herein in the specification and in the claims, should be understood to mean “either or both” of the elements so conjoined, i.e., elements that are conjunctively present in some cases and disjunctively present in other cases. Multiple elements listed with “and/or” should be construed in the same fashion, i.e., “one or more” of the elements so conjoined. Other elements may optionally be present other than the elements specifically identified by the “and/or” clause, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, a reference to “A and/or B”, when used in conjunction with open-ended language such as “comprising” can refer, in one embodiment, to A only (optionally including elements other than B); in another embodiment, to B only (optionally including elements other than A); in yet another embodiment, to both A and B (optionally including other elements); etc.

[0059] As used herein in the specification and in the claims, “or” should be understood to have the same meaning as “and/or” as defined above. For example, when separating

items in a list, “or” or “and/or” shall be interpreted as being inclusive, i.e., the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted items. Only terms clearly indicated to the contrary, such as “only one of” or “exactly one of,” or, when used in the claims, “consisting of,” will refer to the inclusion of exactly one element of a number or list of elements. In general, the term “or” as used herein shall only be interpreted as indicating exclusive alternatives (i.e. “one or the other but not both”) when preceded by terms of exclusivity, such as “either,” “one of,” “only one of,” or “exactly one of.” “Consisting essentially of,” when used in the claims, shall have its ordinary meaning as used in the field of patent law.

[0060] As used herein, the terms “approximately” or “about” in reference to a number are generally taken to include numbers that fall within a range of 5% in either direction (greater than or less than) the number unless otherwise stated or otherwise evident from the context (except where such number would exceed 100% of a possible value). Where ranges are stated, the endpoints are included within the range unless otherwise stated or otherwise evident from the context.

EXAMPLES

Example 1—Edible Vaccines Against Seasonal Influenza

[0061] The following example describes a novel vaccine for the seasonal influenza. The vaccines are made using the following steps: (1) edible cells are engineered to produce hemagglutinin (HA) virus-like particles, (2) transfected cells are expanded in a bioreactor to a target density and virus-like particle yield, and (3) cells are harvested and formulated into a food product (e.g., smoothies, minced meat) at the correct dosage.

Advantages:

[0062] The vaccines described in this example combine the benefits of three technologies: (1) recombinant-based vaccines, (2) plant-based edible vaccines, and (3) cell-based food production. The benefits and limitations of each of these technologies is described below.

[0063] 1. Recombinant-based vaccines—The flu vaccine is generally manufactured in inoculated chicken eggs, which can produce 15 µg of vaccine per 10 mL of fluid (i.e., one egg) (Centers for Disease Control and Prevention, 2019). Three influenza subtypes (A, H1N1; A H3N2, and B) are combined to create a trivalent inactivated influenza vaccine. The flu vaccine is also produced as a cell-based vaccines via infection of mammalian cell cultures. Both of these methods produce a live virus. Alternatively, the flu vaccine can be produced as a subunit recombinant vaccine via genetically engineered cells. Recombinant vaccine production offers increased production speed and reduced allergenicity over egg-based and cell-based vaccines (Vela Ramirez et al., 2017).

[0064] The baculovirus-insect expression system is advantageous for recombinant vaccine production due to its simple design and the ability of insect cells to produce post-transcriptional modifications. Flublok, a recombinant flu vaccine produce in insect cells, was approved by the Food and Drug Administration (FDA) in 2013. Flublok is

administered as an intramuscular injection. A single dose contains 135 μg of trivalent vaccine (i.e., 45 μg of each of 3 full-length recombinant hemagglutinin proteins). The proteins are expressed from the baculovirus vector in *Spodoptera frugiperda* (i.e., fall armyworm) cells. The antigens are extracted from the cell culture and purified via chromatography. The cloning, expression and production process takes less than two months. Other key benefits include high antigen yields, high levels of quality control, and comprehensive research. Limitations of recombinant-based vaccines include that they require purification, produce no mucosal immunity, and require administration by healthcare personnel.

[0065] 2. Edible plant-based vaccines—Oral vaccines can take the form of lyophilized powders that are reconstituted in a single liquid (Vaxchora), multiple liquids (Rotarix, RotaTeq), or provided in capsules (Vivotif). Edible vaccines are also being developed in the form of transgenic plants that are engineered to produce antigens against disease and can be consumed to stimulate mucosal and systemic immunity. For example, vaccines against hepatitis B, Norwalk virus, rabies, and HIV have been expressed in tobacco plants, potatoes, lettuce, tomatoes, and maize (Mishra et al., 2008). In clinical trials, 100 g of raw potato expressing heat-labile enterotoxin B (3.7-15.7 $\mu\text{g/g}$) were shown to induce immunity. To create an edible vaccine, an antigen that can induce an immune response against the target disease is identified, and a gene encoding the antigen is cloned into a transfer vector, commonly *Agrobacterium tumefaciens* (Concha et al., 2017). The antigen-encoding gene is integrated into the plant genome and is expressed in the plant tissue. Key benefits of edible plant-based vaccines include combined mucosal and systemic immunity, self-administration, and no time-consuming and costly purification steps. Limitations of these vaccines include variability in antigen concentration, differences in plant versus human glycosylation patterns, and a lack of comprehensive research.

[0066] 3. Cell-based food—Recently, advances in biotechnology have been applied to the generation of novel foods (e.g., animal-free dairy proteins, recombinant leghemoglobin, cultured meat). Cultured meat is produced by isolating skeletal muscle and adipose-specific stem cells from livestock species, expanding the cells in cultures of xenogen-free growth medium, and differentiating the cells into tissue on food-grade scaffolds (Datar and Betti, 2010). The first proof-of-concept cultured meat was a beef burger constructed from 40 billion bovine muscle cells at Maastricht University in 2013. Today, there are dozens of companies working to commercialize cultured meat. Key benefits of cell-based foods include sustainable production, reduction of foodborne illness, and improved animal welfare (Fraser et al., 2018; Post, 2012). Challenges include achieving large-scale production and reaching price parity with traditional products.

[0067] The edible cell-based vaccines described herein are cultured foods that combine many benefits of recombinant-based and plant-based vaccines (e.g., high yields, quality control, dual immunity, self-administration, no purification). By using a cell-based food production approach, we ensure that our production process is safe, sustainable, and humane. Further, use of this technology for a therapeutic application circumvents the scalability and cost obstacles of cell-based food production, as the target market allows for smaller

scale production and higher price points than would be required to meet consumer meat demands.

[0068] The vaccines described in this example also avoid several key limitations of three technologies: (1) inconsistent dosage, (2) limited efficacy, (3) patient compliance, and (4) cost.

[0069] 1. Dosage consistency—The edible cell-based vaccines will have therapeutic dosage consistency. Edible plant-based vaccines are currently being developed, but their main limitation is dosage inconsistency. Antigen concentrations vary within and between individual plants and between plant generations. For example, in human clinical trials, potato vectors contained between 3.7-15.7 μg of antigen per gram of potato. In contrast, the cultured meat used in our vaccines will be produced in a similar manner to cell-based vaccines, allowing antigen concentrations to be standardized.

[0070] 2. Efficacy—The edible cell-based vaccines will stimulate strong immunity. Edible plant-based vaccines comprising virus-like particle (VLP) formulations have demonstrated success in eliciting broad and long-lasting immunity against various pathogens (Mishra et al., 2008). However, humans cannot digest cellulose, which may limit antigen delivery along the gastrointestinal tract. For our cultured meat vectors, bioavailability should be much higher, as VLPs can be engineered to resist degradation until they reach the small intestine and penetrate the mucosal barrier (Schneider-Ohrum and Ross, 2012).

[0071] 3. Patient compliance—The edible cell-based vaccines will provide pain-free and pill-free administration. Edible vaccines will result in higher patient compliance because they provide an immunization option for populations that have an aversion to needles (20% of adults) or have difficulty swallowing pills (40% of American adults) (Cook, 2016; Schiele et al., 2013). Our cultured meat-based vaccines may also have compliance benefits when compared with existing plant-based vaccines, as cooking and antigen concentration limitations of plant-based vaccines may require patients to eat larger amounts of unappetizing foods (e.g., 100 g of raw potato) (Tacket et al., 2000).

[0072] 4. Cost—The edible cell-based vaccines could incur a lower cost on producers, healthcare systems, and patients. Elimination of purification steps, less stringent storage and transportation requirements, and self-administration all result in lower costs. Moreover, there is already economic pressure for cultured meat to be cost-competitive with conventional products. As resources are developed for more cost-effective production of non-therapeutic cultured meat, these advances will 1 reduce the cost of vaccine-supplemented foods produced through similar methods.

Engineer muscle cells to produce hemagglutinin virus-like particles (HA VLPs). Muscle precursor cells isolated from *Manduca sexta* (caterpillar) and *Bos taurus* (cow) will be engineered to synthesize HA VLPs via transposon-mediated transgenesis. Insect and bovine cells will be proliferated and differentiated as described previously (Baryshyan et al., 2012; Simsa et al., 2019). We will evaluate growth kinetics and differentiation efficiency in non-engineered and engineered cells to determine the effect of HA VLP production on muscle cell behavior.

[0073] Characterize yield, stability, and efficacy of HA VLPs using in vi&o models. Yield, stability and efficacy of HA VLPs will be quantified for both cell types at three points: (a) after proliferation, (b) after differentiation, and (c) after simulated cooking. Stability and efficacy will be evalu-

ated with the aid of three novel in vitro assays: (1) an in vitro simulated digestion to assess VLP stability along the gastrointestinal tract, (2) an in vitro intestine model developed by our group to ensure VLP transportation across the mucosal barrier, and (3) an ALS assay to analyze VLP efficacy via ELISA for antibodies secreted by in vitro lymphocytes (Chang and Sack, 2001).

Methods:

[0074] Muscle cell culture. Insect embryonic precursor cells (EPCs) will be isolated as described previously (Baryshyan et al., 2012). The cells will be isolated from *Manduca sexta* (tobacco hornworm) embryos and cultured in xenogen-free growth medium (Donaldson and Shuler, 1998) supplemented with methoprene. For differentiation experiments, medium will be supplemented with 1 $\mu\text{g/mL}$ of the insect molting hormone 20-hydroxyecdysone (20-HEXRubio et al., 2019). Bovine muscle satellite cells will be isolated from the semitendinosus of a young beef cow as described previously (Simsa et al., 2019). Cells will be expanded on flasks coated with iMatrix recombinant laminin-511, fed basal medium supplemented with 20% fetal bovine serum and 1 ng/mL fibroblast growth factor 2, and differentiated in low-serum medium.

[0075] Transposon-mediated transgenesis. Influenza HA gene sequences from three viruses (i.e., H1N1, H3N2, and H5N1) will be codon optimized for bovine or insect cell expression, synthesized, and cloned into Sleeping Beauty transposon vectors under control of the constitutive promoters CMV and Ac5 for mammalian and insect expression, respectively (Kowarz et al., 2015; Shoji et al., 2008). A trivalent VLP will be generated by linking HA sequences with 2A ribosomal-skipping sequences to enable simultaneous expression of all HA fragments under a single promoter (Szymczak and Vignali, 2005). All genes will be linked via 2A sequences to genes for green fluorescent protein (GFP) and puromycin resistance. Cloned transposon vectors will be co-delivered to cells alongside a Sleeping Beauty transposase vector using a lipofection reagent protocol, as previously utilized by our lab (Stout et al.; Zayed et al., 2004). Stably transfected cells will be selected for with puromycin treatment and verified by detection of GFP expression.

[0076] Cell expansion. Insect cells will be incubated at 25° C. without carbon dioxide, medium will be refreshed once a week, and cells will be passaged at 90% confluency. Bovine cells will be incubated at 37° C. with 5% carbon dioxide, medium will be refreshed every other day, and cells will be passaged at 70% confluency. Growth kinetics will be analyzed via the CyQuant proliferation assay.

[0077] Cell differentiation. Cells will be differentiated using 20-HE supplementation (insect) or low-serum differentiation medium (bovine) for at least 7 days. Differentiation efficiency will be assessed by immunostaining for myosin heavy chain (MHC) and cell nuclei. MHC expression, myotube length, and fusion index will be quantified by Fiji image analysis.

[0078] Thermal treatment. To simulate cooking, differentiated tissues will be cooked in boiling water (100° C.) until they reach a temperature of 70° C. (i.e., the recommended temperature for cooking meat). Samples will be chilled at 4° C. for 24 hours before VLP analysis.

[0079] Western blot & SDS-PAGE. VLPs will be extracted from cell cultures and purified through ultracentrifugation and gradient iodixanol purification. These meth-

ods have been previously used to extract and analyze HA VLPs produced in insect and mammalian cell culture (Thompson et al., 2015). Purified samples will be loaded on a Tris-Glycine gel and run for 40 minutes at 200 V. The protein will be transferred to a nitrocellulose membrane, blocked, and incubated overnight with a primary anti-HA monoclonal antibody and an HRP-conjugated secondary antibody for 1 hour. Yield will be quantified via densitometric analysis. To analyze VLP size, purified VLPs (10 μg) will be loaded on a 12% SDS-PAGE gel and stained with Coomassie blue.

[0080] In vitro digestion. VLP cell cultures will be exposed to an in vitro digestion assay designed to mimic the dynamic conditions of the gastrointestinal tract. Cells will be incubated in buffers emulating the pH of the salivary (2 minutes at 37° C.), gastric (2 hours at 37° C.) and intestinal (2 hours at 37° C.) phases of digestion (Marseglia et al., 2019). Compositions are as follows: in vitro salivary fluid will be a 6.2 pH buffer supplemented with amylase, in vitro gastric fluid will be a 3.0 pH buffer supplemented with pepsin, and in vitro intestinal fluid will be a 7.0 pH buffer supplemented with pancreatin and bile solution. Upon digestion, stability of VLPs will be assessed via transmission electron microscopy, dynamic light scattering, and the following bioavailability and efficacy assays.

[0081] Transmission electron microscopy. Purified VLP samples will be diluted and placed on 200 Hex carbon coated and glow-discharged grids. Grids will be washed and incubated with 1.5% uranyl formate. After drying, grids will be imaged with a transmission electron microscope.

[0082] Dynamic light scattering. Purified VLPs will be analyzed with a NanoBrook Zeta analyzer at a concentration of 500 $\mu\text{g/mL}$.

[0083] In vitro bioavailability assay. To study uptake in intestinal cells, we will employ a Caco-2 bioavailability assay. VLP-containing engineered tissue will be subjected to in vitro digestion as described above. VLP yield within the digested solution will be determined as described above. The digested solution will then be applied to a cell culture of Caco-2 cells. Caco-2 cells will be cultured on Transwell inserts, seeded at 500,000 cells/cm², and fed RPMI 1640 medium supplemented with 10% fetal bovine serum and 1% antibiotic. Caco-2 cells will be treated with 5-150 μg of HA VLPs, cell viability will be quantified via MTT assay, and VLP uptake by Caco-2 cells will be measured by immunostaining (Lazorova et al.).

[0084] Vaccine efficacy assay. It has been reported that the induction of cytokine expression, in either primary human peripheral blood mononuclear cells (PMBCs) or the THP-1 line of human monocytic cells, may serve as a valid in vitro assay of vaccine efficacy (Desheva et al., 2019). We will employ a similar strategy. PMBCs or THP-1 cells will be cultured in 96-well plates. Preparations of digested VLP-expressing tissue will be generated as described above. PMBC or THP-1 cultures will be treated with serial dilutions of digested tissue at each stage of digestion. Purified VLPs will be used as a positive control. At several time points (4 hr, 24 hr, and 7 days after treatment), cell culture supernatant will be collected for ELISA of secreted cytokines, and cells will be collected and subjected to total RNA extraction for q-PCR analysis of cytokine mRNA expression levels. We will assess the cytokines IFN γ , TNF α , IL-2, and IL-6. As purified VLPs have been used clinically as vaccines, the cytokine expression profile of purified VLP-treated cells will

be used as our gold standard. The expression profiles generated from digested engineered meat-treated cells will be compared to this gold standard to determine if a similar immuno-stimulatory response can be achieved.

REFERENCES

- [0085] Ashok, A., Brison, M., and LeTallec, Y. (2017). Improving cold chain systems: Challenges and solutions. *Vaccine* 35, 2217-2223. doi:10.1016/j.vaccine.2016.08.045.
- [0086] Baryshyan, A. L., Woods, W., Trimmer, B. A., and Kaplan, D. L. (2012). Isolation and Maintenance-Free Culture of Contractile Myotubes from *Manduca sexta* Embryos. *PLoS One* 7, e31598. doi:10.1371/journal.pone.0031598.
- [0087] Bonanni, P., Picazo, J. J., and Remy, V. (2015). The intangible benefits of vaccination—what is the true economic value of vaccination? *J. Mark. Access Heal. Policy* 3, 26964. doi:10.3402/jmahp.v3.26964.
- [0088] Centers for Disease Control and Prevention (2019). How Influenza (Flu) Vaccines Are Made. *Seas. Infl.* Available at: <https://www.cdc.gov/flu/prevent/how-flu-vaccine-made.htm> [Accessed Feb. 15, 2020].
- [0089] Centers for Disease Control and Prevention (2020). Disease Burden of Influenza. *Seas. Infl.* Available at: <https://www.cdc.gov/flu/about/burden/rndex.html> [Accessed Feb. 15, 2020].
- [0090] Chang, H. S., and Sack, D. A. (2001). Development of a novel in vitro assay (ALS assay) for evaluation of vaccine-induced antibody secretion from circulating mucosal lymphocytes. *Clin. Diagn. Lab. Immunol.* 8, 482-488. doi:10.1128/CDLI.8.3.482-488.2001.
- [0091] Chen, J. R., Liu, Y. M., Tseng, Y. C., and Ma, C. (2020). Better influenza vaccines: An industry perspective. *J. Biomed. Sci.* 27. doi:10.1186/s12929-020-0626-6.
- [0092] Concha, C., Cañas, R., Macuer, J., Torres, M. J., Herrada, A. A., Jamett, F., et al. (2017). Disease Prevention: An Opportunity to Expand Edible Plant-Based Vaccines? doi:10.3390/vaccines5020014.
- [0093] Cook, L. S. (2016). Needle phobia. *J. Infus. Nurs.* 39, 273-279. doi:10.1097/NAN.0000000000000184.
- [0094] D'Aoust, M. A., Couture, M. M. J., Charland, N., Trepanier, S., Landry, N., Ors, F., et al. (2010). The production of hemagglutinin-based virus-like particles in plants: A rapid, efficient and safe response to pandemic influenza. *Plant Biotechnol. J.* 8, 607-619. doi:10.1111/j.1467-7652.2009.00496.x.
- [0095] Datar, I., and Betti, M. (2010). Possibilities for an in vitro meat production system. *Innov. Food Sci. Emerg. Technol.* 11, 13-22. doi:10.1016/j.ifset.2009.10.007.
- [0096] Desheva, Y. A., Leontieva, G. F., Kramskaya, T. A., Landgraf, G. O., Sychev, I. A., Rekstin, A. R., et al. (2019). Factors of early protective action of live influenza vaccine combined with recombinant bacterial polypeptides against homologous and heterologous influenza infection. *Heliyon* 5, e01154. doi:10.1016/j.heliyon.2019.e01154.
- [0097] Donaldson, M. S., and Shuler, M. L. (1998). Low-Cost Serum-Free Medium for the BTI-Tn5B1-4 Insect Cell Line. *Biotechnol. Prog.* 14, 573-579. doi:10.1021/bp9800541.
- [0098] Fraser, R. Z., Shitut, M., Agrawal, P., Mendes, O., and Klapholz, S. (2018). Safety Evaluation of Soy Leghemoglobin Protein Preparation Derived From *Pichia pastoris*, Intended for Use as a Flavor Catalyst in Plant-Based Meat. *Int. J. Toxicol.* 37, 241-262. doi:10.1177/1091581818766318.
- [0099] Kowarz, E., Loscher, D., and Marschalek, R. (2015). Optimized Sleeping Beauty transposons rapidly generate stable transgenic cell lines. *Biotechnol. J.* 10, 647-653. doi:10.1002/biot.201400821.
- [0100] Lazorova, L., Engstrom, A., and Sijlander, A. Transport of an influenza virus vaccine formulation (iscom) in Caco-2 cells.
- [0101] Marseglia, A., Dellafiora, L., Prandi, B., Lolli, V., Sforza, S., Cozzini, P., et al. (2019). Simulated gastrointestinal digestion of cocoa: Detection of resistant peptides and in silico/in vitro prediction of their ace inhibitory activity. *Nutrients* 11. doi:10.3390/nu11050985.
- [0102] Mishra, N., Gupta, N., Khatri, K., Goyal, A. K., and Vyas, S. P. (2008). Edible vaccines: A new approach to oral immunization.
- [0103] Ortiz, J. R., and Neuzil, K. M. (2019). Influenza Immunization in Low- and Middle-Income Countries: Preparing for Next-Generation Influenza Vaccines. *J. Infect. Dis.* 219, S97-S106. doi:10.1093/infdis/jiz024.
- [0104] Post, M. J. (2012). Cultured Meat from Stem Cells: Challenges and Prospects. *Meat Sci.* 92, 297-301. doi:10.1016/j.meatsci.2012.04.008.
- [0105] Rubio, N. R., Fish, K. D., Trimmer, B. A., and Kaplan, D. L. (2019). In Vitro Insect Muscle for Tissue Engineering Applications. *ACS Biomater. Sci. Eng.* 5, 1071-1082. doi:10.1021/acsbiomaterials.8b01261.
- [0106] Schiele, J. T., Quinzler, R., Klimm, H. D., Pruszydlo, M. G., and Haefeli, W. E. (2013). Difficulties swallowing solid oral dosage forms in a general practice population: Prevalence, causes, and relationship to dosage forms. *Eur. J. Clin. Pharmacol.* 69, 937-948. doi:10.1007/s00228-012-1417-0.
- [0107] Schneider-Ohrum, K., and Ross, T. M. (2012). Virus-like particles for antigen delivery at mucosal surfaces. *Curr. Top. Microbiol. Immunol.* 354, 53-73. doi:10.1007/82_2011_135.
- [0108] Serradell, M. C., Rupil, L. L., Martino, R. A., Prucca, C. G., Carranza, P. G., Saura, A., et al. (2019). Efficient oral vaccination by bioengineering virus-like particles with protozoan surface proteins. *Nat. Commun.* 10, 361. doi:10.1038/s41467-018-08265-9.
- [0109] Shoji, Y., Chichester, J. A., Bi, H., Musiyuchuk, K., de la Rosa, P., Goldschmidt, L., et al. (2008). Plant-expressed HA as a seasonal influenza vaccine candidate. *Vaccine* 26, 2930-2934. doi:10.1016/j.vaccine.2008.03.045.
- [0110] Simsa, R., Yuen, J., Stout, A., Rubio, N., Fogelstrand, P., and Kaplan, D. L. (2019). Extracellular heme proteins influence bovine myosatellite cell proliferation and the color of cell-based meat. *Foods* 8. doi:10.3390/foods8100521.
- [0111] Stout, A. J., Mirliani, A. B., Soule-Albridge, E. L., Cohen, J. M., and Kaplan, D. L. Engineering carotenoid production in mammalian cells for nutritionally enhanced cell-cultured foods. *Rev.*
- [0112] Szymczak, A. L., and Vignali, D. A. (2005). Development of 2A peptide-based strategies in the design of multicistronic vectors. *Expert Opin. Biol. Ther.* 5, 627-638. doi:10.1517/14712598.5.5.627.
- [0113] Tacket, C. O., Mason, H. S., Losonsky, G., Estes, M. K., Levine, M. M., and Arntzen, C. J. (2000). Human

Immune Responses to a Novel Norwalk Virus Vaccine Delivered in Transgenic Potatoes. *J. Infect. Dis.* 182, 302-305. doi:10.1086/315653.

[0114] Thompson, C. M., Petiot, E., Mullick, A., Aucoin, M. G., Henry, O., and Kamen, A. A. (2015). Critical assessment of influenza VLP production in Sf9 and HEK293 expression systems. *BMC Biotechnol.* 15, 31. doi:10.1186/s12896-015-0152-x.

[0115] Vela Ramirez, J. E., Sharpe, L. A., and Peppas, N. A. (2017). Current State and Challenges in Developing Oral Vaccines. *Adv. Drug Deliv. Rev.* 114, 116-131. doi:10.1016/j.addr.2017.04.008.

[0116] World Health Organization (2015). World Health Statistics 2012. World Health Organization.

[0117] Young, E. (2018). 41 Percent of Americans Do Not Intend to Get a Flu Shot this Season. *Natl. Opin. Res. Cent.*

[0118] Zayed, H., Izsvik, Z., Walisko, O., and Ivics, Z. (2004). Development of Hyperactive Sleeping Beauty Transposon Vectors by Mutational Analysis. *Mol. Ther.* 9, 292-304. doi:10.1016/J.YMTHE.2003.11.024.

Example 2—Antigens for Edible Vaccines Against Various Diseases

[0119] As is described in Example 1, edible cell-based vaccines against influenza can be created by engineering cells to express influenza antigens, such hemagglutinin (HA), neuraminidase (NA), matrix protein 1 (M1), and/or matrix protein 2 (M2). The amino acid sequences of HA subtypes 1-16 are provided as SEQ ID NOs:1-16, respectively; the amino acid sequences of NA subtypes 1-9 are provided as SEQ ID NOs:17-25, respectively; and the amino acid sequences of M1 and M2 are provided as SEQ ID NOs:26-27, respectively. Further, the amino acid sequences of the HA polypeptide from H1N1 (A/Hawaii/70/2019), H3N2 (A/Kansas/14/2017), and H5N1 (A/Egypt/2321-NAMRU3/2007) are provided as SEQ ID NOs:28-30, respectively.

[0120] Additionally, the edible cell-based vaccine platform described herein could also be used to generate vac-

cines against coronaviruses such as severe acute respiratory syndrome coronavirus (SARS-CoV), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and Middle East respiratory syndrome coronavirus (MERS-CoV). Such vaccines can be created by engineering cells to express coronavirus antigens, such as the spike (S), envelope (E), membrane (M), and/or receptor binding domain (RBD) proteins. The amino acid sequences of the S, E, and M proteins of SARS-CoV are provided as SEQ ID NOs:31-33, respectively; the amino acid sequences of the S, E, M, and RBD proteins of SARS-CoV-2 are provided as SEQ ID NOs:34-37, respectively; and the amino acid sequences of the S, E, and M proteins of MERS-CoV are provided as SEQ ID NOs:38-40, respectively.

[0121] The edible cell-based vaccine platform could also be used to generate vaccines against hepatitis B. Such vaccines can be created by engineering cells to express hepatitis B antigens, such major hepatitis B surface antigens (HBsAg), which are classified as large (L-HBsAg), middle (M-HBsAg), and small (S-HBsAg) proteins. The amino acid sequences of L-HBsAg, M-HBsAg, and S-HBsAg from hepatitis B are provided as SEQ ID NOs:41-43, respectively.

[0122] The edible cell-based vaccine platform could also be used to generate vaccines against human papillomavirus (HPV). Such vaccines can be created by engineering cells to express HPV antigens, such as L1. The amino acid sequences of the L1 protein from HPV type 6, 11, 16, and 18 are provided as SEQ ID NOs:44-47, respectively.

[0123] The edible cell-based vaccine platform could also be used to generate vaccines against human parvovirus. Such vaccines can be created by engineering cells to express parvovirus antigens such as viral protein 1 (VP1) and/or viral protein 2 (VP2). The amino acid sequences of VP1 and VP2 are provided as SEQ ID NOs:48 and 49, respectively.

[0124] The edible cell-based vaccine platform could also be used to generate vaccines against Norwalk virus. Such vaccines can be created by engineering cells to express Norwalk virus antigens such as capsid protein (CP). The amino acid sequence of CP is provided as SEQ ID NO: 50.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 50

<210> SEQ ID NO 1

<211> LENGTH: 565

<212> TYPE: PRT

<213> ORGANISM: Influenza A virus

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(565)

<223> OTHER INFORMATION: HA Type 1

<400> SEQUENCE: 1

Met Lys Ala Asn Leu Leu Val Leu Leu Cys Ala Leu Ala Ala Asp
1 5 10 15

Ala Asp Thr Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Asp Thr
20 25 30

Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His Ser Val Asn
35 40 45

Leu Leu Glu Asp Ser His Asn Gly Lys Leu Cys Arg Leu Lys Gly Ile
50 55 60

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Ala	Pro	Leu	Gln	Leu	Gly	Lys	Cys	Asn	Ile	Ala	Gly	Trp	Leu	Leu	Gly	
65					70					75					80	
Asn	Pro	Glu	Cys	Asp	Pro	Leu	Leu	Pro	Val	Arg	Ser	Trp	Ser	Tyr	Ile	
				85					90					95		
Val	Glu	Thr	Pro	Asn	Ser	Glu	Asn	Gly	Ile	Cys	Tyr	Pro	Gly	Asp	Phe	
			100					105					110			
Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val	Ser	Ser	Phe	
		115					120					125				
Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Glu	Ser	Ser	Trp	Pro	Asn	His	Asn	
	130					135					140					
Thr	Asn	Gly	Val	Thr	Ala	Ala	Cys	Ser	His	Glu	Gly	Lys	Ser	Ser	Phe	
145					150					155					160	
Tyr	Arg	Asn	Leu	Leu	Trp	Leu	Thr	Glu	Lys	Glu	Gly	Ser	Tyr	Pro	Lys	
			165						170					175		
Leu	Lys	Asn	Ser	Tyr	Val	Asn	Lys	Lys	Gly	Lys	Glu	Val	Leu	Val	Leu	
		180						185					190			
Trp	Gly	Ile	His	His	Pro	Pro	Asn	Ser	Lys	Glu	Gln	Gln	Asn	Leu	Tyr	
		195					200					205				
Gln	Asn	Glu	Asn	Ala	Tyr	Val	Ser	Val	Val	Thr	Ser	Asn	Tyr	Asn	Arg	
	210					215					220					
Arg	Phe	Thr	Pro	Glu	Ile	Ala	Glu	Arg	Pro	Lys	Val	Arg	Asp	Gln	Ala	
225				230						235					240	
Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Leu	Lys	Pro	Gly	Asp	Thr	Ile	
			245						250					255		
Ile	Phe	Glu	Ala	Asn	Gly	Asn	Leu	Ile	Ala	Pro	Met	Tyr	Ala	Phe	Ala	
		260					265						270			
Leu	Ser	Arg	Gly	Phe	Gly	Ser	Gly	Ile	Ile	Thr	Ser	Asn	Ala	Ser	Met	
	275					280						285				
His	Glu	Cys	Asn	Thr	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Ala	Ile	Asn	Ser	
	290				295						300					
Ser	Leu	Pro	Tyr	Gln	Asn	Ile	His	Pro	Val	Thr	Ile	Gly	Glu	Cys	Pro	
305				310						315					320	
Lys	Tyr	Val	Arg	Ser	Ala	Lys	Leu	Arg	Met	Val	Thr	Gly	Leu	Arg	Asn	
			325						330					335		
Ile	Pro	Ser	Ile	Gln	Ser	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	
		340						345					350			
Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Ile	Asp	Gly	Trp	Tyr	Gly	Tyr	His	
	355					360						365				
His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Gln	Lys	Ser	Thr	
	370				375						380					
Gln	Asn	Ala	Ile	Asn	Gly	Ile	Thr	Asn	Lys	Val	Asn	Thr	Val	Ile	Glu	
385				390						395					400	
Lys	Met	Asn	Ile	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	Lys	Leu	
			405						410					415		
Glu	Lys	Arg	Met	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	
		420					425						430			
Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	
	435					440						445				
Arg	Thr	Leu	Asp	Phe	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	
	450					455					460					

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Val	Lys	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	
465					470					475					480	
Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Glu	Cys	Met	Glu	Ser	Val	Arg	
				485					490					495		
Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ser	Lys	Leu	Asn	
			500					505					510			
Arg	Glu	Lys	Val	Asp	Gly	Val	Lys	Leu	Glu	Ser	Met	Gly	Ile	Tyr	Gln	
		515					520					525				
Ile	Leu	Ala	Ile	Tyr	Ser	Thr	Val	Ala	Ser	Ser	Leu	Val	Leu	Leu	Val	
	530					535					540					
Ser	Leu	Gly	Ala	Ile	Ser	Phe	Trp	Met	Cys	Ser	Asn	Gly	Ser	Leu	Gln	
545					550					555					560	
Cys	Arg	Ile	Cys	Ile												
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<212> TYPE: PRT																
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<221> NAME/KEY: MISC_FEATURE																
<222> LOCATION: (1)..(562)																
<223> OTHER INFORMATION: HA Type 2																
<400> SEQUENCE: 2																
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Gln	Ile	Cys	Ile	Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Glu	Met	Val	Asp	
			20					25					30			
Thr	Ile	Leu	Glu	Arg	Asn	Val	Thr	Val	Thr	His	Ala	Lys	Asp	Ile	Leu	
		35				40						45				
Glu	Lys	Thr	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu	Asn	Gly	Ile	Pro	Pro	
	50					55					60					
Leu	Glu	Leu	Gly	Asp	Cys	Ser	Ile	Ala	Gly	Trp	Leu	Leu	Gly	Asn	Pro	
65				70					75						80	
Glu	Cys	Asp	Arg	Leu	Leu	Ser	Val	Pro	Glu	Trp	Ser	Tyr	Ile	Met	Glu	
			85						90					95		
Lys	Glu	Asn	Pro	Arg	Asp	Gly	Leu	Cys	Tyr	Pro	Gly	Ser	Phe	Asn	Asp	
			100					105						110		
Tyr	Glu	Glu	Leu	Lys	His	Leu	Leu	Ser	Ser	Val	Lys	His	Phe	Glu	Lys	
		115					120					125				
Val	Lys	Ile	Leu	Pro	Lys	Asp	Arg	Trp	Thr	Gln	His	Thr	Thr	Thr	Gly	
	130					135						140				
Gly	Ser	Arg	Ala	Cys	Ala	Val	Ser	Gly	Asn	Pro	Ser	Phe	Phe	Arg	Asn	
145					150					155					160	
Met	Val	Trp	Leu	Thr	Lys	Lys	Gly	Ser	Asp	Tyr	Pro	Val	Ala	Lys	Gly	
			165						170					175		
Ser	Tyr	Asn	Asn	Thr	Ser	Gly	Glu	Gln	Met	Leu	Ile	Ile	Trp	Gly	Val	
			180					185					190			
His	His	Pro	Asn	Asp	Glu	Thr	Glu	Gln	Arg	Thr	Leu	Tyr	Gln	Asn	Val	
		195					200					205				
Gly	Thr	Tyr	Val	Ser	Val	Gly	Thr	Ser	Thr	Leu	Asn	Lys	Arg	Ser	Thr	
	210					215					220					
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<210> SEQ ID NO 3
<211> LENGTH: 566
<212> TYPE: PRT
<213> ORGANISM: Influenza A virus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(566)
<223> OTHER INFORMATION: HA Type 3

<400> SEQUENCE: 3
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Met	Lys	Thr	Ile	Ile	Ala	Leu	Ser	Tyr	Ile	Phe	Cys	Leu	Ala	Leu	Gly	
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Gln	Asp	Leu	Pro	Gly	Asn	Asp	Asn	Ser	Thr	Ala	Thr	Leu	Cys	Leu	Gly	
			20					25					30			
His	His	Ala	Val	Pro	Asn	Gly	Thr	Leu	Val	Lys	Thr	Ile	Thr	Asp	Asp	
		35					40					45				
Gln	Ile	Glu	Val	Thr	Asn	Ala	Thr	Glu	Leu	Val	Gln	Ser	Ser	Ser	Thr	
	50					55					60					
Gly	Lys	Ile	Cys	Asn	Asn	Pro	His	Arg	Ile	Leu	Asp	Gly	Ile	Asp	Cys	
65					70				75						80	
Thr	Leu	Ile	Asp	Ala	Leu	Leu	Gly	Asp	Pro	His	Cys	Asp	Val	Phe	Gln	
				85				90						95		
Asn	Glu	Thr	Trp	Asp	Leu	Phe	Val	Glu	Arg	Ser	Lys	Ala	Phe	Ser	Asn	
			100					105					110			
Cys	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser	Leu	Arg	Ser	Leu	Val	
		115					120					125				
Ala	Ser	Ser	Gly	Thr	Leu	Glu	Phe	Ile	Thr	Glu	Gly	Phe	Thr	Trp	Thr	
	130					135					140					
Gly	Val	Thr	Gln	Asn	Gly	Gly	Ser	Asn	Ala	Cys	Lys	Arg	Gly	Pro	Gly	
145					150					155					160	
Ser	Gly	Phe	Phe	Ser	Arg	Leu	Asn	Trp	Leu	Thr	Lys	Ser	Gly	Ser	Thr	
				165				170						175		
Tyr	Pro	Val	Leu	Asn	Val	Thr	Met	Pro	Asn	Asn	Asp	Asn	Phe	Asp	Lys	
			180					185					190			
Leu	Tyr	Ile	Trp	Gly	Val	His	His	Pro	Ser	Thr	Asn	Gln	Glu	Gln	Thr	
		195					200					205				
Ser	Leu	Tyr	Val	Gln	Ala	Ser	Gly	Arg	Val	Thr	Val	Ser	Thr	Arg	Arg	
	210					215					220					
Ser	Gln	Gln	Thr	Ile	Ile	Pro	Asn	Ile	Glu	Ser	Arg	Pro	Trp	Val	Arg	
225					230					235					240	
Gly	Leu	Ser	Ser	Arg	Ile	Ser	Ile	Tyr	Trp	Thr	Ile	Val	Lys	Pro	Gly	
				245				250						255		
Asp	Val	Leu	Val	Ile	Asn	Ser	Asn	Gly	Asn	Leu	Ile	Ala	Pro	Arg	Gly	
		260						265					270			
Tyr	Phe	Lys	Met	Arg	Thr	Gly	Lys	Ser	Ser	Ile	Met	Arg	Ser	Asp	Ala	
		275					280					285				
Pro	Ile	Asp	Thr	Cys	Ile	Ser	Glu	Cys	Ile	Thr	Pro	Asn	Gly	Ser	Ile	
	290					295					300					
Pro	Asn	Asp	Lys	Pro	Phe	Gln	Asn	Val	Asn	Lys	Ile	Thr	Tyr	Gly	Ala	
305					310					315					320	
Cys	Pro	Lys	Tyr	Val	Lys	Gln	Asn	Thr	Leu	Lys	Leu	Ala	Thr	Gly	Met	
				325				330						335		
Arg	Asn	Val	Pro	Glu	Lys	Gln	Thr	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	
			340					345					350			
Gly	Phe	Ile	Glu	Asn	Gly	Trp	Glu	Gly	Met	Ile	Asp	Gly	Trp	Tyr	Gly	
		355					360					365				
Phe	Arg	His	Gln	Asn	Ser	Glu	Gly	Thr	Gly	Gln	Ala	Ala	Asp	Leu	Lys	
	370					375					380					
Ser	Thr	Gln	Ala	Ala	Ile	Asp	Gln	Ile	Asn	Gly	Lys	Leu	Asn	Arg	Val	
385					390					395				400		
Ile	Glu	Lys	Thr	Asn	Glu	Lys	Phe	His	Gln	Ile	Glu	Lys	Glu	Phe	Ser	

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405																410				415			
Glu	Val	Glu	Gly	Arg	Ile	Gln	Asp	Leu	Glu	Lys	Tyr	Val	Glu	Asp	Thr								
420								425				430											
Lys	Ile	Asp	Leu	Trp	Ser	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Ala	Leu	Glu								
435								440				445											
Asn	Gln	His	Thr	Ile	Asp	Leu	Thr	Asp	Ser	Glu	Met	Asn	Lys	Leu	Phe								
450								455				460											
Glu	Lys	Thr	Arg	Arg	Gln	Leu	Arg	Glu	Asn	Ala	Glu	Asp	Met	Gly	Asn								
465								470				475				480							
Gly	Cys	Phe	Lys	Ile	Tyr	His	Lys	Cys	Asp	Asn	Ala	Cys	Ile	Glu	Ser								
485								490				495											
Ile	Arg	Asn	Gly	Thr	Tyr	Asp	His	Asp	Val	Tyr	Arg	Asp	Glu	Ala	Leu								
500								505				510											
Asn	Asn	Arg	Phe	Gln	Ile	Lys	Gly	Val	Glu	Leu	Lys	Ser	Gly	Tyr	Lys								
515								520				525											
Asp	Trp	Ile	Leu	Trp	Ile	Ser	Phe	Ala	Ile	Ser	Cys	Phe	Leu	Leu	Cys								
530								535				540											
Val	Val	Leu	Leu	Gly	Phe	Ile	Met	Trp	Ala	Cys	Gln	Arg	Gly	Asn	Ile								
545								550				555				560							
Arg	Cys	Asn	Ile	Cys	Ile																		
565																							
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<223> OTHER INFORMATION: HA Type 4																							
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1				5				10				15											
Gln	Asn	Tyr	Thr	Gly	Asn	Pro	Val	Ile	Cys	Leu	Gly	His	His	Ala	Val								
20				25				30															
Pro	Asn	Gly	Thr	Met	Val	Lys	Thr	Leu	Thr	Asp	Asp	Gln	Val	Glu	Val								
35				40				45															
Val	Thr	Ala	Gln	Glu	Leu	Val	Glu	Ser	Gln	His	Leu	Pro	Glu	Leu	Cys								
50				55				60															
Pro	Ser	Pro	Leu	Arg	Leu	Val	Asp	Gly	Gln	Thr	Cys	Asp	Ile	Val	Asn								
65				70				75				80											
Gly	Ala	Leu	Gly	Ser	Pro	Gly	Cys	Asp	His	Leu	Asn	Gly	Ala	Glu	Trp								
85				90				95															
Asp	Val	Phe	Ile	Glu	Arg	Pro	Thr	Ala	Val	Asp	Thr	Cys	Tyr	Pro	Phe								
100				105				110															
Asp	Val	Pro	Asp	Tyr	Gln	Ser	Leu	Arg	Ser	Ile	Leu	Ala	Asn	Asn	Gly								
115				120				125															
Lys	Phe	Glu	Phe	Ile	Ala	Glu	Glu	Phe	Gln	Trp	Asn	Thr	Val	Lys	Gln								
130				135				140															
Asn	Gly	Lys	Ser	Gly	Ala	Cys	Lys	Arg	Ala	Asn	Val	Asn	Asp	Phe	Phe								
145				150				155				160											
Asn	Arg	Leu	Asn	Trp	Leu	Thr	Lys	Ser	Asp	Gly	Asn	Ala	Tyr	Pro	Leu								
165								170				175											

Gln	Asn	Leu	Thr	Lys	Val	Asn	Asn	Gly	Asp	Tyr	Ala	Arg	Leu	Tyr	Ile	
			180				185						190			
Trp	Gly	Val	His	His	Pro	Ser	Thr	Asp	Thr	Glu	Gln	Thr	Asn	Leu	Tyr	
		195				200					205					
Glu	Asn	Asn	Pro	Gly	Arg	Val	Thr	Val	Ser	Thr	Gln	Thr	Ser	Gln	Thr	
		210				215					220					
Ser	Val	Val	Pro	Asn	Ile	Gly	Ser	Arg	Pro	Trp	Val	Arg	Gly	Gln	Ser	
225					230					235					240	
Gly	Arg	Ile	Ser	Phe	Tyr	Trp	Thr	Ile	Val	Glu	Pro	Gly	Asp	Leu	Ile	
			245						250					255		
Val	Phe	Asn	Thr	Ile	Gly	Asn	Leu	Ile	Ala	Pro	Arg	Gly	His	Tyr	Lys	
			260						265					270		
Leu	Asn	Ser	Gln	Lys	Lys	Ser	Thr	Ile	Leu	Asn	Thr	Ala	Val	Pro	Ile	
		275					280					285				
Gly	Ser	Cys	Val	Ser	Lys	Cys	His	Thr	Asp	Arg	Gly	Ser	Ile	Ser	Thr	
		290					295					300				
Thr	Lys	Pro	Phe	Gln	Asn	Ile	Ser	Arg	Ile	Ser	Ile	Gly	Asp	Cys	Pro	
305					310					315					320	
Lys	Tyr	Val	Lys	Gln	Gly	Ser	Leu	Lys	Leu	Ala	Thr	Gly	Met	Arg	Asn	
			325						330					335		
Ile	Pro	Glu	Lys	Ala	Thr	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	
			340						345					350		
Ile	Glu	Asn	Gly	Trp	Gln	Gly	Leu	Ile	Asp	Gly	Trp	Tyr	Gly	Phe	Arg	
		355					360					365				
His	Gln	Asn	Ala	Glu	Gly	Thr	Gly	Thr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	
370					375					380						
Gln	Ala	Ala	Ile	Asp	Gln	Ile	Asn	Gly	Lys	Leu	Asn	Arg	Leu	Ile	Glu	
385					390					395					400	
Lys	Thr	Asn	Glu	Lys	Tyr	His	Gln	Ile	Glu	Lys	Glu	Phe	Glu	Gln	Val	
			405						410					415		
Glu	Gly	Arg	Ile	Gln	Asp	Leu	Glu	Lys	Tyr	Val	Glu	Asp	Thr	Lys	Ile	
		420					425					430				
Asp	Leu	Trp	Ser	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Ala	Leu	Glu	Asn	Gln	
		435					440					445				
His	Thr	Ile	Asp	Val	Thr	Asp	Ser	Glu	Met	Asn	Lys	Leu	Phe	Glu	Arg	
450					455					460						
Val	Arg	Arg	Gln	Leu	Arg	Glu	Asn	Ala	Glu	Asp	Lys	Gly	Asn	Gly	Cys	
465					470					475					480	
Phe	Glu	Ile	Phe	His	Gln	Cys	Asp	Asn	Ser	Cys	Ile	Glu	Ser	Ile	Arg	
			485						490					495		
Asn	Gly	Thr	Tyr	Asp	His	Asp	Ile	Tyr	Arg	Asp	Glu	Ala	Ile	Asn	Asn	
			500						505					510		
Arg	Phe	Gln	Ile	Gln	Gly	Val	Lys	Leu	Thr	Gln	Gly	Tyr	Lys	Asp	Ile	
		515					520					525				
Ile	Leu	Trp	Ile	Ser	Phe	Ser	Ile	Ser	Cys	Phe	Leu	Leu	Val	Ala	Leu	
530					535					540						
Leu	Leu	Ala	Phe	Ile	Leu	Trp	Ala	Cys	Gln	Asn	Gly	Asn	Ile	Arg	Cys	
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Gln	Ile	Cys	Ile													

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Asp	Gln	Ile	Cys	Ile	Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Glu	Gln	Val
			20					25					30		
Asp	Thr	Ile	Met	Glu	Lys	Asn	Val	Thr	Val	Thr	His	Ala	Gln	Asp	Ile
			35				40					45			
Leu	Glu	Arg	Thr	His	Asn	Gly	Lys	Leu	Cys	Asp	Leu	Asn	Gly	Val	Lys
	50					55					60				
Pro	Leu	Ile	Leu	Arg	Asp	Cys	Ser	Val	Ala	Gly	Trp	Leu	Leu	Gly	Asn
65					70					75					80
Pro	Met	Cys	Asp	Glu	Phe	Ile	Asn	Val	Pro	Glu	Trp	Ser	Tyr	Ile	Val
				85					90					95	
Glu	Lys	Ala	Ser	Pro	Ala	Asn	Asp	Leu	Cys	Tyr	Pro	Gly	Asn	Phe	Asn
			100					105					110		
Asp	Tyr	Glu	Glu	Leu	Lys	His	Leu	Leu	Ser	Arg	Ile	Asn	His	Phe	Glu
			115				120					125			
Lys	Ile	Gln	Ile	Ile	Pro	Lys	Ser	Ser	Trp	Ser	Asn	His	Asp	Ala	Ser
	130					135					140				
Ser	Gly	Val	Ser	Ser	Ala	Cys	Pro	Tyr	Leu	Gly	Arg	Ser	Ser	Phe	Phe
145					150					155					160
Arg	Asn	Val	Val	Trp	Leu	Ile	Lys	Lys	Asn	Ser	Ala	Tyr	Pro	Thr	Ile
				165					170					175	
Lys	Arg	Ser	Tyr	Asn	Asn	Thr	Asn	Gln	Glu	Asp	Leu	Leu	Val	Leu	Trp
			180					185					190		
Gly	Ile	His	His	Pro	Asn	Asp	Ala	Ala	Glu	Gln	Thr	Lys	Leu	Tyr	Gln
			195				200					205			
Asn	Pro	Thr	Thr	Tyr	Ile	Ser	Val	Gly	Thr	Ser	Thr	Leu	Asn	Gln	Arg
	210					215					220				
Leu	Val	Pro	Glu	Ile	Ala	Thr	Arg	Pro	Lys	Val	Asn	Gly	Gln	Ser	Gly
225					230					235					240
Arg	Met	Glu	Phe	Phe	Trp	Thr	Ile	Leu	Lys	Pro	Asn	Asp	Ala	Ile	Asn
				245					250					255	
Phe	Glu	Ser	Asn	Gly	Asn	Phe	Ile	Ala	Pro	Glu	Tyr	Ala	Tyr	Lys	Ile
			260					265					270		
Val	Lys	Lys	Gly	Asp	Ser	Thr	Ile	Met	Lys	Ser	Glu	Leu	Glu	Tyr	Gly
		275					280					285			
Asn	Cys	Asn	Thr	Lys	Cys	Gln	Thr	Pro	Met	Gly	Ala	Ile	Asn	Ser	Ser
	290					295					300				
Met	Pro	Phe	His	Asn	Ile	His	Pro	Leu	Thr	Ile	Gly	Glu	Cys	Pro	Lys
305					310					315					320
Tyr	Val	Lys	Ser	Asn	Arg	Leu	Val	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Thr
				325					330					335	
Pro	Gln	Arg	Glu	Arg	Arg	Arg	Lys	Lys	Arg	Gly	Leu	Phe	Gly	Ala	Ile
			340					345					350		

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Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Gln	Gly	Met	Val	Asp	Gly	Trp	Tyr	
	355						360					365				
Gly	Tyr	His	His	Ser	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Lys	
	370					375					380					
Glu	Ser	Thr	Gln	Lys	Ala	Ile	Asp	Gly	Val	Thr	Asn	Lys	Val	Asn	Ser	
385					390					395					400	
Ile	Ile	Asn	Lys	Met	Asn	Thr	Gln	Phe	Glu	Ala	Val	Gly	Arg	Glu	Phe	
			405						410					415		
Asn	Asn	Leu	Glu	Arg	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Met	Glu	Asp	
		420						425					430			
Gly	Phe	Leu	Asp	Val	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Met	
	435						440					445				
Glu	Asn	Glu	Arg	Thr	Leu	Asp	Phe	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	
	450					455					460					
Tyr	Asp	Lys	Val	Arg	Leu	Gln	Leu	Arg	Asp	Asn	Ala	Lys	Glu	Leu	Gly	
465					470					475					480	
Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Glu	Cys	Met	Glu	
			485						490					495		
Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Gln	Tyr	Ser	Glu	Glu	Ala	
			500					505					510			
Arg	Leu	Asn	Arg	Glu	Glu	Ile	Ser	Gly	Val	Lys	Leu	Glu	Ser	Met	Gly	
	515						520					525				
Thr	Tyr	Gln	Ile	Leu	Ser	Ile	Tyr	Ser	Thr	Val	Ala	Ser	Ser	Leu	Ala	
	530					535					540					
Leu	Ala	Ile	Met	Val	Ala	Gly	Leu	Ser	Leu	Trp	Met	Cys	Ser	Asn	Gly	
545				550						555					560	
Ser	Leu	Gln	Cys	Arg	Ile	Cys	Ile									
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1				5					10					15		
Asp	Lys	Ile	Cys	Ile	Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Thr	Gln	Val	
		20						25					30			
Asp	Thr	Ile	Leu	Glu	Lys	Asn	Val	Thr	Val	Thr	His	Ser	Val	Glu	Leu	
	35						40					45				
Leu	Glu	Asn	Gln	Lys	Glu	Glu	Arg	Phe	Cys	Lys	Ile	Leu	Asn	Lys	Ala	
	50					55					60					
Pro	Leu	Asp	Leu	Arg	Gly	Cys	Thr	Ile	Glu	Gly	Trp	Ile	Leu	Gly	Asn	
65				70					75						80	
Pro	Gln	Cys	Asp	Leu	Leu	Leu	Gly	Asp	Gln	Ser	Trp	Ser	Tyr	Ile	Val	
			85					90					95			
Glu	Arg	Pro	Thr	Ala	Gln	Asn	Gly	Ile	Cys	Tyr	Pro	Gly	Val	Leu	Asn	
		100					105						110			

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Glu	Val	Glu	Glu	Leu	Lys	Ala	Leu	Ile	Gly	Ser	Gly	Glu	Arg	Val	Glu	
		115					120					125				
Arg	Phe	Glu	Met	Phe	Pro	Lys	Ser	Thr	Trp	Ala	Gly	Val	Asp	Thr	Ser	
	130					135					140					
Ser	Gly	Val	Thr	Arg	Ala	Cys	Pro	Tyr	Asn	Thr	Gly	Ser	Ser	Phe	Tyr	
145					150					155					160	
Arg	Asn	Leu	Leu	Trp	Ile	Ile	Lys	Thr	Lys	Ser	Ala	Ala	Tyr	Pro	Val	
				165					170					175		
Ile	Lys	Gly	Thr	Tyr	Asn	Asn	Thr	Gly	Lys	Gln	Pro	Ile	Leu	Tyr	Phe	
			180					185					190			
Trp	Gly	Val	His	His	Pro	Pro	Asp	Thr	Asn	Glu	Gln	Asn	Thr	Leu	Tyr	
		195					200					205				
Gly	Ser	Gly	Asp	Arg	Tyr	Val	Arg	Met	Gly	Thr	Glu	Ser	Met	Asn	Phe	
	210					215					220					
Ala	Lys	Ser	Pro	Glu	Ile	Ala	Ala	Arg	Pro	Ala	Val	Asn	Gly	Gln	Arg	
225					230					235					240	
Gly	Arg	Ile	Asp	Tyr	Tyr	Trp	Ser	Val	Leu	Lys	Pro	Gly	Glu	Thr	Leu	
			245						250					255		
Asn	Val	Glu	Ser	Asn	Gly	Asn	Leu	Ile	Ala	Pro	Trp	Tyr	Ala	Tyr	Arg	
			260					265					270			
Phe	Val	Ser	Thr	Ile	Asn	Lys	Gly	Ala	Val	Phe	Lys	Ser	Asn	Leu	Pro	
		275					280					285				
Ile	Glu	Asn	Cys	Asp	Ala	Thr	Cys	Gln	Thr	Ile	Ala	Gly	Val	Leu	Arg	
	290					295					300					
Thr	Asn	Lys	Thr	Phe	Gln	Asn	Val	Ser	Pro	Leu	Trp	Ile	Gly	Glu	Cys	
305					310					315					320	
Pro	Lys	Tyr	Val	Lys	Ser	Gly	Ser	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg	
				325					330					335		
Asn	Val	Pro	Gln	Ile	Glu	Thr	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	
			340					345					350			
Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Ile	Asp	Gly	Trp	Tyr	Gly	Tyr	
		355					360					365				
His	His	Glu	Asn	Ser	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Arg	Glu	Ser	
	370					375					380					
Thr	Gln	Lys	Ala	Ile	Asp	Gly	Ile	Thr	Asn	Lys	Val	Asn	Ser	Ile	Ile	
385					390					395					400	
Asp	Lys	Met	Asn	Thr	Gln	Phe	Glu	Ala	Val	Asp	His	Glu	Phe	Ser	Asn	
				405					410					415		
Leu	Glu	Arg	Arg	Ile	Asp	Asn	Leu	Asn	Lys	Arg	Met	Glu	Asp	Gly	Phe	
			420					425					430			
Leu	Asn	Val	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	
		435					440					445				
Glu	Arg	Thr	Leu	Asp	Leu	His	Asp	Ala	Asn	Val	Lys	Asn	Leu	Tyr	Glu	
	450					455					460					
Lys	Val	Lys	Ser	Gln	Leu	Arg	Asp	Asn	Ala	Asn	Asp	Leu	Gly	Asn	Gly	
465					470					475					480	
Cys	Phe	Glu	Phe	Trp	His	Lys	Cys	Asp	Asn	Glu	Cys	Ile	Glu	Ser	Val	
				485					490					495		
Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Gln	Asp	Glu	Ser	Lys	Leu	
			500					505					510			
Asn	Arg	Gln	Glu	Ile	Glu	Ser	Val	Lys	Leu	Glu	Asn	Leu	Gly	Val	Tyr	

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515					520					525						
Gln	Ile	Leu	Ala	Ile	Tyr	Ser	Thr	Val	Ser	Ser	Ser	Leu	Val	Leu	Val	
530					535					540						
Gly	Leu	Ile	Ile	Ala	Met	Gly	Leu	Trp	Met	Cys	Ser	Asn	Gly	Ser	Met	
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Gln Cys Arg Ile Cys Ile																
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1	5				10				15							
Asn	Ala	Asp	Lys	Ile	Cys	Leu	Gly	His	His	Ala	Val	Ser	Asn	Gly	Thr	
			20				25				30					
Lys	Val	Asn	Thr	Leu	Thr	Glu	Arg	Gly	Val	Glu	Val	Val	Asn	Ala	Thr	
		35			40			45								
Glu	Thr	Val	Glu	Arg	Thr	Asn	Val	Pro	Arg	Ile	Cys	Ser	Lys	Gly	Lys	
50				55			60									
Arg	Thr	Val	Asp	Leu	Gly	Gln	Cys	Gly	Leu	Leu	Gly	Thr	Ile	Thr	Gly	
65				70			75			80						
Pro	Pro	Gln	Cys	Asp	Gln	Phe	Leu	Glu	Phe	Ser	Ala	Asp	Leu	Ile	Ile	
			85				90				95					
Glu	Arg	Arg	Glu	Gly	Ser	Asp	Val	Cys	Tyr	Pro	Gly	Lys	Phe	Val	Asn	
			100				105				110					
Glu	Glu	Ala	Leu	Arg	Gln	Ile	Leu	Arg	Glu	Ser	Gly	Gly	Ile	Asp	Lys	
115				120			125									
Glu	Thr	Met	Gly	Phe	Thr	Tyr	Ser	Gly	Ile	Arg	Thr	Asn	Gly	Ala	Thr	
130				135			140									
Ser	Ala	Cys	Arg	Arg	Ser	Gly	Ser	Ser	Phe	Tyr	Ala	Glu	Met	Lys	Trp	
145				150			155			160						
Leu	Leu	Ser	Asn	Thr	Asp	Asn	Ala	Ala	Phe	Pro	Gln	Met	Thr	Lys	Ser	
			165				170				175					
Tyr	Lys	Asn	Thr	Arg	Lys	Asp	Pro	Ala	Leu	Ile	Ile	Trp	Gly	Ile	His	
		180			185			190								
His	Ser	Gly	Ser	Thr	Thr	Glu	Gln	Thr	Lys	Leu	Tyr	Gly	Ser	Gly	Asn	
195				200			205									
Lys	Leu	Ile	Thr	Val	Gly	Ser	Ser	Asn	Tyr	Gln	Gln	Ser	Phe	Val	Pro	
210				215			220									
Ser	Pro	Glu	Ala	Arg	Pro	Gln	Val	Asn	Gly	Gln	Ser	Gly	Arg	Ile	Asp	
225				230			235			240						
Phe	His	Trp	Leu	Met	Leu	Asn	Pro	Asn	Asp	Thr	Val	Thr	Phe	Ser	Phe	
			245				250				255					
Asn	Gly	Ala	Phe	Ile	Ala	Pro	Asp	Arg	Ala	Ser	Phe	Leu	Arg	Gly	Lys	
			260				265				270					
Ser	Met	Gly	Ile	Gln	Ser	Gly	Val	Gln	Val	Asp	Ala	Asn	Cys	Glu	Gly	
275				280			285									

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Asp	Cys	Tyr	His	Ser	Gly	Gly	Thr	Ile	Ile	Ser	Asn	Leu	Pro	Phe	Gln	
290						295					300					
Asn	Ile	Asn	Ser	Arg	Ala	Val	Gly	Lys	Cys	Pro	Arg	Tyr	Val	Lys	Gln	
305					310					315					320	
Glu	Ser	Leu	Leu	Leu	Ala	Thr	Gly	Met	Lys	Asn	Val	Pro	Glu	Ile	Pro	
				325					330					335		
Lys	Gly	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Asn	Gly	
			340					345					350			
Trp	Glu	Gly	Leu	Ile	Asp	Gly	Trp	Tyr	Gly	Phe	Arg	His	Gln	Asn	Ala	
	355						360					365				
Gln	Gly	Glu	Gly	Thr	Ala	Ala	Asp	Tyr	Lys	Ser	Thr	Gln	Ser	Ala	Ile	
	370						375					380				
Asp	Gln	Val	Thr	Gly	Lys	Leu	Asn	Arg	Leu	Ile	Glu	Lys	Thr	Asn	Gln	
385					390					395					400	
Gln	Phe	Lys	Leu	Ile	Asp	Asn	Glu	Phe	Thr	Glu	Val	Glu	Lys	Gln	Ile	
			405						410					415		
Gly	Asn	Val	Ile	Asn	Trp	Thr	Arg	Asp	Ser	Met	Thr	Glu	Val	Trp	Ser	
		420						425					430			
Tyr	Asn	Ala	Glu	Leu	Leu	Val	Ala	Met	Glu	Asn	Gln	His	Thr	Ile	Asp	
	435						440					445				
Leu	Ala	Asp	Ser	Glu	Met	Asn	Lys	Leu	Tyr	Glu	Arg	Val	Lys	Arg	Gln	
	450					455					460					
Leu	Arg	Glu	Asn	Ala	Glu	Glu	Asp	Gly	Thr	Gly	Cys	Phe	Glu	Ile	Phe	
465					470					475					480	
His	Lys	Cys	Asp	Asp	Asp	Cys	Met	Ala	Ser	Ile	Arg	Asn	Asn	Thr	Tyr	
			485						490					495		
Asp	His	Ser	Lys	Tyr	Arg	Glu	Glu	Ala	Met	Gln	Asn	Arg	Ile	Gln	Ile	
		500						505					510			
Asp	Pro	Val	Lys	Leu	Ser	Ser	Gly	Tyr	Lys	Asp	Val	Ile	Leu	Trp	Phe	
	515						520					525				
Ser	Phe	Gly	Ala	Ser	Cys	Phe	Ile	Leu	Leu	Ala	Ile	Ala	Met	Gly	Leu	
	530					535					540					
Val	Phe	Ile	Cys	Val	Lys	Asn	Gly	Asn	Met	Arg	Cys	Thr	Ile	Cys	Ile	
545				550						555					560	
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1				5					10					15		
Asp	Arg	Ile	Cys	Ile	Gly	Tyr	Gln	Ser	Asn	Asn	Ser	Thr	Asp	Thr	Val	
		20					25						30			
Asn	Thr	Leu	Ile	Glu	Gln	Asn	Val	Pro	Val	Thr	Gln	Thr	Met	Glu	Leu	
	35					40						45				
Val	Glu	Thr	Glu	Lys	His	Pro	Ala	Tyr	Cys	Asn	Thr	Asp	Leu	Gly	Ala	
50					55					60						

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Pro	Leu	Glu	Leu	Arg	Asp	Cys	Lys	Ile	Glu	Ala	Val	Ile	Tyr	Gly	Asn	
65					70					75					80	
Pro	Lys	Cys	Asp	Ile	His	Leu	Lys	Asp	Gln	Gly	Trp	Ser	Tyr	Ile	Val	
				85					90					95		
Glu	Arg	Pro	Ser	Ala	Pro	Glu	Gly	Met	Cys	Tyr	Pro	Gly	Ser	Val	Glu	
			100					105					110			
Asn	Leu	Glu	Glu	Leu	Arg	Phe	Val	Phe	Ser	Ser	Ala	Ala	Ser	Tyr	Lys	
		115					120					125				
Arg	Ile	Arg	Leu	Phe	Asp	Tyr	Ser	Arg	Trp	Asn	Val	Thr	Arg	Ser	Gly	
	130					135					140					
Thr	Ser	Lys	Ala	Cys	Asn	Ala	Ser	Thr	Gly	Gly	Gln	Ser	Phe	Tyr	Arg	
145					150					155					160	
Ser	Ile	Asn	Trp	Leu	Thr	Lys	Lys	Glu	Pro	Asp	Thr	Tyr	Asp	Phe	Asn	
				165					170					175		
Glu	Gly	Ala	Tyr	Val	Asn	Asn	Glu	Asp	Gly	Asp	Ile	Ile	Phe	Leu	Trp	
			180					185					190			
Gly	Ile	His	His	Pro	Pro	Asp	Thr	Lys	Glu	Gln	Thr	Thr	Leu	Tyr	Lys	
		195					200					205				
Asn	Ala	Asn	Thr	Leu	Ser	Ser	Val	Thr	Thr	Asn	Thr	Ile	Asn	Arg	Ser	
		210				215					220					
Phe	Gln	Pro	Asn	Ile	Gly	Pro	Arg	Pro	Leu	Val	Arg	Gly	Gln	Gln	Gly	
225					230					235					240	
Arg	Met	Asp	Tyr	Tyr	Trp	Gly	Ile	Leu	Lys	Arg	Gly	Glu	Thr	Leu	Lys	
				245					250					255		
Ile	Arg	Thr	Asn	Gly	Asn	Leu	Ile	Ala	Pro	Glu	Phe	Gly	Tyr	Leu	Leu	
			260					265					270			
Lys	Gly	Glu	Ser	Tyr	Gly	Arg	Ile	Ile	Gln	Asn	Glu	Asp	Ile	Pro	Ile	
		275					280					285				
Gly	Asn	Cys	Asn	Thr	Lys	Cys	Gln	Thr	Tyr	Ala	Gly	Ala	Ile	Asn	Ser	
	290					295					300					
Ser	Lys	Pro	Phe	Gln	Asn	Ala	Ser	Arg	His	Tyr	Met	Gly	Glu	Cys	Pro	
305					310					315					320	
Lys	Tyr	Val	Lys	Lys	Ala	Ser	Leu	Arg	Leu	Ala	Val	Gly	Leu	Arg	Asn	
				325					330					335		
Thr	Pro	Ser	Val	Glu	Pro	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	
			340					345					350			
Ile	Glu	Gly	Gly	Trp	Ser	Gly	Met	Ile	Asp	Gly	Trp	Tyr	Gly	Phe	His	
		355					360					365				
His	Ser	Asn	Ser	Glu	Gly	Thr	Gly	Met	Ala	Ala	Asp	Gln	Lys	Ser	Thr	
	370					375					380					
Gln	Glu	Ala	Ile	Asp	Lys	Ile	Thr	Asn	Lys	Val	Asn	Asn	Ile	Val	Asp	
385					390					395					400	
Lys	Met	Asn	Arg	Glu	Phe	Glu	Val	Val	Asn	His	Glu	Phe	Ser	Glu	Val	
				405					410					415		
Glu	Lys	Arg	Ile	Asn	Met	Ile	Asn	Asp	Lys	Ile	Asp	Asp	Gln	Ile	Glu	
			420					425					430			
Asp	Leu	Trp	Ala	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Gln	
		435					440					445				
Lys	Thr	Leu	Asp	Glu	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Phe	Asp	Glu	
	450					455					460					
Val	Lys	Arg	Arg	Leu	Ser	Ala	Asn	Ala	Ile	Asp	Ala	Gly	Asn	Gly	Cys	

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465					470					475					480
Phe	Asp	Ile	Leu	His	Lys	Cys	Asp	Asn	Glu	Cys	Met	Glu	Thr	Ile	Lys
				485					490					495	
Asn	Gly	Thr	Tyr	Asp	His	Lys	Glu	Tyr	Glu	Glu	Glu	Ala	Lys	Leu	Glu
			500					505					510		
Arg	Ser	Lys	Ile	Asn	Gly	Val	Lys	Leu	Glu	Glu	Asn	Thr	Thr	Tyr	Lys
		515					520					525			
Ile	Leu	Ser	Ile	Tyr	Ser	Thr	Val	Ala	Ala	Ser	Leu	Cys	Leu	Ala	Ile
	530					535					540				
Leu	Ile	Ala	Gly	Gly	Leu	Ile	Leu	Gly	Met	Gln	Asn	Gly	Ser	Cys	Arg
545					550					555					560
Cys	Met	Phe	Cys	Ile											
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1				5					10					15	
Asn	Ala	Asp	Lys	Ile	Cys	Ile	Gly	Tyr	Gln	Ser	Thr	Asn	Ser	Thr	Glu
			20					25					30		
Thr	Val	Asp	Thr	Leu	Thr	Glu	Ser	Asn	Val	Pro	Val	Thr	His	Thr	Lys
		35					40					45			
Glu	Leu	Leu	His	Thr	Glu	His	Asn	Gly	Met	Leu	Cys	Ala	Thr	Asp	Leu
	50					55					60				
Gly	His	Pro	Leu	Ile	Leu	Asp	Thr	Cys	Thr	Ile	Glu	Gly	Leu	Ile	Tyr
65				70					75						80
Gly	Asn	Pro	Ser	Cys	Asp	Ile	Leu	Leu	Gly	Gly	Lys	Glu	Trp	Ser	Tyr
				85					90					95	
Ile	Val	Glu	Arg	Ser	Ser	Ala	Val	Asn	Gly	Met	Cys	Tyr	Pro	Gly	Asn
		100						105					110		
Val	Glu	Asn	Leu	Glu	Glu	Leu	Arg	Ser	Leu	Phe	Ser	Ser	Ala	Lys	Ser
		115					120					125			
Tyr	Lys	Arg	Ile	Gln	Ile	Phe	Pro	Asp	Lys	Thr	Trp	Asn	Val	Thr	Tyr
	130					135					140				
Ser	Gly	Thr	Ser	Arg	Ala	Cys	Ser	Asn	Ser	Phe	Tyr	Arg	Ser	Met	Arg
145				150						155					160
Trp	Leu	Thr	His	Lys	Ser	Asn	Ser	Tyr	Pro	Phe	Gln	Asn	Ala	His	Tyr
			165					170						175	
Thr	Asn	Asn	Glu	Arg	Glu	Asn	Ile	Leu	Phe	Met	Trp	Gly	Ile	His	His
		180						185					190		
Pro	Pro	Thr	Asp	Thr	Glu	Gln	Thr	Asp	Leu	Tyr	Lys	Asn	Ala	Asp	Thr
		195					200					205			
Thr	Thr	Ser	Val	Thr	Thr	Glu	Asp	Ile	Asn	Arg	Thr	Phe	Lys	Pro	Val
	210					215					220				
Ile	Gly	Pro	Arg	Pro	Leu	Val	Asn	Gly	Gln	Gln	Gly	Arg	Ile	Asp	Tyr
225					230					235					240

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Tyr	Trp	Ser	Val	Leu	Lys	Pro	Gly	Gln	Thr	Leu	Arg	Ile	Arg	Ser	Asn	
				245					250					255		
Gly	Asn	Leu	Ile	Ala	Pro	Trp	Tyr	Gly	His	Val	Leu	Thr	Gly	Glu	Ser	
			260					265					270			
His	Gly	Arg	Ile	Leu	Lys	Thr	Asp	Leu	Asn	Asn	Gly	Asn	Cys	Val	Val	
		275					280					285				
Gln	Cys	Gln	Thr	Glu	Lys	Gly	Gly	Leu	Asn	Thr	Thr	Leu	Pro	Phe	His	
	290					295					300					
Asn	Ile	Ser	Lys	Tyr	Ala	Phe	Gly	Asn	Cys	Pro	Lys	Tyr	Val	Gly	Val	
305					310					315					320	
Lys	Ser	Leu	Lys	Leu	Pro	Val	Gly	Leu	Arg	Asn	Val	Pro	Ala	Val	Ser	
				325					330					335		
Ser	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	
			340					345					350			
Pro	Gly	Leu	Val	Ala	Gly	Trp	Tyr	Gly	Phe	Gln	His	Ser	Asn	Asp	Gln	
		355					360					365				
Gly	Val	Gly	Met	Ala	Ala	Asp	Lys	Gly	Ser	Thr	Gln	Lys	Ala	Ile	Asp	
	370					375					380					
Lys	Ile	Thr	Ser	Lys	Val	Asn	Asn	Ile	Ile	Asp	Lys	Met	Asn	Lys	Gln	
385					390					395					400	
Tyr	Glu	Val	Ile	Asp	His	Glu	Phe	Asn	Glu	Leu	Glu	Ala	Arg	Leu	Asn	
				405					410					415		
Met	Ile	Asn	Asn	Lys	Ile	Asp	Asp	Gln	Ile	Gln	Asp	Ile	Trp	Ala	Tyr	
			420					425					430			
Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Gln	Lys	Thr	Leu	Asp	Glu	
		435				440					445					
His	Asp	Ala	Asn	Val	Asn	Asn	Leu	Tyr	Asn	Lys	Val	Lys	Arg	Ala	Leu	
	450					455					460					
Gly	Ser	Asn	Ala	Val	Glu	Asp	Gly	Asn	Gly	Cys	Phe	Glu	Leu	Tyr	His	
465					470					475					480	
Lys	Cys	Asp	Asp	Gln	Cys	Met	Glu	Thr	Ile	Arg	Asn	Gly	Thr	Tyr	Asp	
				485					490					495		
Arg	Gln	Lys	Tyr	Gln	Glu	Glu	Ser	Arg	Leu	Glu	Arg	Gln	Lys	Ile	Glu	
			500					505					510			
Gly	Val	Lys	Leu	Glu	Ser	Glu	Gly	Thr	Tyr	Lys	Ile	Leu	Thr	Ile	Tyr	
		515					520					525				
Ser	Thr	Val	Ala	Ser	Ser	Leu	Val	Leu	Ala	Met	Gly	Phe	Ala	Ala	Phe	
	530					535					540					
Leu	Phe	Trp	Ala	Met	Ser	Asn	Gly	Ser	Cys	Arg	Cys	Asn	Ile	Cys	Ile	
545					550					555					560	
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1				5					10					15		

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Leu	Asp	Arg	Ile	Cys	Leu	Gly	His	His	Ala	Val	Ala	Asn	Gly	Thr	Ile	
			20					25					30			
Val	Lys	Thr	Leu	Thr	Asn	Glu	Gln	Glu	Glu	Val	Thr	Asn	Ala	Thr	Glu	
		35					40					45				
Thr	Val	Glu	Ser	Thr	Asn	Leu	Asn	Lys	Leu	Cys	Met	Lys	Gly	Arg	Ser	
		50				55					60					
Tyr	Lys	Asp	Leu	Gly	Asn	Cys	His	Pro	Val	Gly	Met	Leu	Ile	Gly	Thr	
65					70					75					80	
Pro	Val	Cys	Asp	Pro	His	Leu	Thr	Gly	Thr	Trp	Asp	Thr	Leu	Ile	Glu	
				85					90					95		
Arg	Glu	Asn	Ala	Ile	Ala	His	Cys	Tyr	Pro	Gly	Ala	Thr	Ile	Asn	Glu	
			100					105						110		
Glu	Ala	Leu	Arg	Gln	Lys	Ile	Met	Glu	Ser	Gly	Gly	Ile	Ser	Lys	Met	
		115					120					125				
Ser	Thr	Gly	Phe	Thr	Tyr	Gly	Ser	Ser	Ile	Thr	Ser	Ala	Gly	Thr	Thr	
		130				135					140					
Lys	Ala	Cys	Met	Arg	Asn	Gly	Gly	Asp	Ser	Phe	Tyr	Ala	Glu	Leu	Lys	
145					150					155					160	
Trp	Leu	Val	Ser	Lys	Thr	Lys	Gly	Gln	Asn	Phe	Pro	Gln	Thr	Thr	Asn	
				165					170					175		
Thr	Tyr	Arg	Asn	Thr	Asp	Thr	Ala	Glu	His	Leu	Ile	Ile	Trp	Gly	Ile	
			180					185					190			
His	His	Pro	Ser	Ser	Thr	Gln	Glu	Lys	Asn	Asp	Leu	Tyr	Gly	Thr	Gln	
		195					200					205				
Ser	Leu	Ser	Ile	Ser	Val	Glu	Ser	Ser	Thr	Tyr	Gln	Asn	Asn	Phe	Val	
		210				215					220					
Pro	Val	Val	Gly	Ala	Arg	Pro	Gln	Val	Asn	Gly	Gln	Ser	Gly	Arg	Ile	
225					230					235					240	
Asp	Phe	His	Trp	Thr	Leu	Val	Gln	Pro	Gly	Asp	Asn	Ile	Thr	Phe	Ser	
				245					250					255		
Asp	Asn	Gly	Gly	Leu	Ile	Ala	Pro	Ser	Arg	Val	Ser	Lys	Leu	Thr	Gly	
			260					265					270			
Arg	Asp	Leu	Gly	Ile	Gln	Ser	Glu	Ala	Leu	Ile	Asp	Asn	Ser	Cys	Glu	
		275					280					285				
Ser	Lys	Cys	Phe	Trp	Arg	Gly	Gly	Ser	Ile	Asn	Thr	Lys	Leu	Pro	Phe	
		290				295					300					
Gln	Asn	Leu	Ser	Pro	Arg	Thr	Val	Gly	Gln	Cys	Pro	Lys	Tyr	Val	Asn	
305					310					315					320	
Gln	Arg	Ser	Leu	Leu	Leu	Ala	Thr	Gly	Met	Arg	Asn	Val	Pro	Glu	Val	
				325					330					335		
Val	Gln	Gly	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Asn	
			340					345					350			
Gly	Trp	Glu	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Phe	Arg	His	Gln	Asn	
		355					360					365				
Ala	Gln	Gly	Thr	Gly	Gln	Ala	Ala	Asp	Tyr	Lys	Ser	Thr	Gln	Ala	Ala	
						375					380					
Ile	Asp	Gln	Ile	Thr	Gly	Lys	Leu	Asn	Arg	Leu	Ile	Glu	Lys	Thr	Asn	
385					390				395						400	
Thr	Glu	Phe	Glu	Ser	Ile	Glu	Ser	Glu	Phe	Ser	Glu	Thr	Glu	His	Gln	
				405					410					415		
Ile	Gly	Asn	Val	Ile	Asn	Trp	Thr	Lys	Asp	Ser	Ile	Thr	Asp	Ile	Trp	

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Gly	Ile	His	His	Pro	Ala	Thr	Leu	Thr	Glu	His	Gln	Asp	Leu	Tyr	Lys	
		195					200					205				
Lys	Asp	Ser	Ser	Tyr	Val	Ala	Val	Gly	Ser	Glu	Thr	Tyr	Asn	Arg	Arg	
	210					215					220					
Phe	Thr	Pro	Glu	Ile	Asn	Thr	Arg	Pro	Arg	Val	Asn	Gly	Gln	Ala	Gly	
225					230					235					240	
Arg	Met	Thr	Phe	Tyr	Trp	Lys	Ile	Val	Lys	Pro	Gly	Glu	Ser	Ile	Thr	
				245					250					255		
Phe	Glu	Ser	Asn	Gly	Ala	Phe	Leu	Ala	Pro	Arg	Tyr	Ala	Phe	Glu	Ile	
			260					265					270			
Val	Ser	Val	Gly	Asn	Gly	Lys	Leu	Phe	Arg	Ser	Glu	Leu	Asn	Ile	Glu	
		275					280					285				
Ser	Cys	Ser	Thr	Lys	Cys	Gln	Thr	Glu	Ile	Gly	Gly	Ile	Asn	Thr	Asn	
	290					295					300					
Lys	Ser	Phe	His	Asn	Val	His	Arg	Asn	Thr	Ile	Gly	Asp	Cys	Pro	Lys	
305					310					315					320	
Tyr	Val	Asn	Val	Lys	Ser	Leu	Lys	Leu	Ala	Thr	Gly	Pro	Arg	Asn	Val	
				325					330					335		
Pro	Ala	Ile	Ala	Ser	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	
			340					345					350			
Glu	Gly	Gly	Trp	Pro	Gly	Leu	Ile	Asn	Gly	Trp	Tyr	Gly	Phe	Gln	His	
		355					360					365				
Arg	Asn	Glu	Glu	Gly	Thr	Gly	Ile	Ala	Ala	Asp	Lys	Glu	Ser	Thr	Gln	
	370					375					380					
Lys	Ala	Ile	Asp	Gln	Ile	Thr	Ser	Lys	Val	Asn	Asn	Ile	Val	Asp	Arg	
385					390					395					400	
Met	Asn	Thr	Asn	Phe	Glu	Ser	Val	Gln	His	Glu	Phe	Ser	Glu	Ile	Glu	
				405					410					415		
Glu	Arg	Ile	Asn	Gln	Leu	Ser	Lys	His	Val	Asp	Asp	Ser	Val	Val	Asp	
			420					425					430			
Ile	Trp	Ser	Tyr	Asn	Ala	Gln	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Lys	
		435					440					445				
Thr	Leu	Asp	Leu	His	Asp	Ser	Asn	Val	Arg	Asn	Leu	His	Glu	Lys	Val	
	450					455					460					
Arg	Arg	Met	Leu	Lys	Asp	Asn	Ala	Lys	Asp	Glu	Gly	Asn	Gly	Cys	Phe	
465					470					475					480	
Thr	Phe	Tyr	His	Lys	Cys	Asp	Asn	Lys	Cys	Ile	Glu	Arg	Val	Arg	Asn	
				485					490					495		
Gly	Thr	Tyr	Asp	His	Lys	Glu	Phe	Glu	Glu	Glu	Ser	Lys	Ile	Asn	Arg	
			500					505					510			
Gln	Glu	Ile	Glu	Gly	Val	Lys	Leu	Asp	Ser	Ser	Gly	Asn	Val	Tyr	Lys	
		515					520					525				
Ile	Leu	Ser	Ile	Tyr	Ser	Cys	Ile	Ala	Ser	Ser	Leu	Val	Leu	Ala	Ala	
	530					535					540					
Leu	Ile	Met	Gly	Phe	Met	Phe	Trp	Ala	Cys	Ser	Asn	Gly	Ser	Cys	Arg	
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Cys	Thr	Ile	Cys	Ile												
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<211> LENGTH: 564
<212> TYPE: PRT

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1				5					10					15					
Tyr	Asp	Lys	Ile	Cys	Ile	Gly	Tyr	Gln	Thr	Asn	Asn	Ser	Thr	Glu	Thr				
			20					25					30						
Val	Asn	Thr	Leu	Ser	Glu	Gln	Asn	Val	Pro	Val	Thr	Gln	Val	Glu	Glu				
			35				40					45							
Leu	Val	His	Arg	Gly	Ile	Asp	Pro	Ile	Leu	Cys	Gly	Thr	Glu	Leu	Gly				
			50			55					60								
Ser	Pro	Leu	Val	Leu	Asp	Asp	Cys	Ser	Leu	Glu	Gly	Leu	Ile	Leu	Gly				
65					70					75					80				
Asn	Pro	Lys	Cys	Asp	Leu	Tyr	Leu	Asn	Gly	Arg	Glu	Trp	Ser	Tyr	Ile				
				85					90					95					
Val	Glu	Arg	Pro	Lys	Glu	Met	Glu	Gly	Val	Cys	Tyr	Pro	Gly	Ser	Ile				
			100					105						110					
Glu	Asn	Gln	Glu	Glu	Leu	Arg	Ser	Leu	Phe	Ser	Ser	Ile	Lys	Lys	Tyr				
			115				120					125							
Glu	Arg	Val	Lys	Met	Phe	Asp	Phe	Thr	Lys	Trp	Asn	Val	Thr	Tyr	Thr				
			130			135					140								
Gly	Thr	Ser	Lys	Ala	Cys	Asn	Asn	Thr	Ser	Asn	Gln	Gly	Ser	Phe	Tyr				
145					150					155					160				
Arg	Ser	Met	Arg	Trp	Leu	Thr	Leu	Lys	Ser	Gly	Gln	Phe	Pro	Val	Gln				
				165					170					175					
Thr	Asp	Glu	Tyr	Lys	Asn	Thr	Arg	Asp	Ser	Asp	Ile	Val	Phe	Thr	Trp				
			180					185					190						
Ala	Ile	His	His	Pro	Pro	Thr	Ser	Asp	Glu	Gln	Val	Lys	Leu	Tyr	Lys				
			195				200					205							
Asn	Pro	Asp	Thr	Leu	Ser	Ser	Val	Thr	Thr	Val	Glu	Ile	Asn	Arg	Ser				
						215					220								
Phe	Lys	Pro	Asn	Ile	Gly	Pro	Arg	Pro	Leu	Val	Arg	Gly	Gln	Gln	Gly				
225					230					235					240				
Arg	Met	Asp	Tyr	Tyr	Trp	Ala	Val	Leu	Lys	Pro	Gly	Gln	Thr	Val	Lys				
				245					250					255					
Ile	Gln	Thr	Asn	Gly	Asn	Leu	Ile	Ala	Pro	Glu	Tyr	Gly	His	Leu	Ile				
			260					265					270						
Thr	Gly	Lys	Ser	His	Gly	Arg	Ile	Leu	Lys	Asn	Asn	Leu	Pro	Met	Gly				
			275				280					285							
Gln	Cys	Val	Thr	Glu	Cys	Gln	Leu	Asn	Glu	Gly	Val	Met	Asn	Thr	Ser				
			290			295					300								
Lys	Pro	Phe	Gln	Asn	Thr	Ser	Lys	His	Tyr	Ile	Gly	Lys	Cys	Pro	Lys				
305					310					315					320				
Tyr	Ile	Pro	Ser	Gly	Ser	Leu	Lys	Leu	Ala	Ile	Gly	Leu	Arg	Asn	Val				
				325					330					335					
Pro	Gln	Val	Gln	Asp	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile				
			340					345					350						
Glu	Gly	Gly	Trp	Pro	Gly	Leu	Val	Ala	Gly	Trp	Tyr	Gly	Phe	Gln	His				
			355				360					365							

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Gln	Asn	Ala	Glu	Gly	Thr	Gly	Ile	Ala	Ala	Asp	Arg	Asp	Ser	Thr	Gln	
	370					375				380						
Arg	Ala	Ile	Asp	Asn	Met	Gln	Asn	Lys	Leu	Asn	Asn	Val	Ile	Asp	Lys	
385					390					395					400	
Met	Asn	Lys	Gln	Phe	Glu	Val	Val	Asn	His	Glu	Phe	Ser	Glu	Val	Glu	
				405					410					415		
Ser	Arg	Ile	Asn	Met	Ile	Asn	Ser	Lys	Ile	Asp	Asp	Gln	Ile	Thr	Asp	
			420					425					430			
Ile	Trp	Ala	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Gln	Lys	
	435						440					445				
Thr	Leu	Asp	Glu	His	Asp	Ala	Asn	Val	Arg	Asn	Leu	His	Asp	Arg	Val	
	450					455					460					
Arg	Arg	Val	Leu	Arg	Glu	Asn	Ala	Ile	Asp	Thr	Gly	Asp	Gly	Cys	Phe	
465					470					475					480	
Glu	Ile	Leu	His	Lys	Cys	Asp	Asn	Asn	Cys	Met	Asp	Thr	Ile	Arg	Asn	
				485					490					495		
Gly	Thr	Tyr	Asn	His	Lys	Glu	Tyr	Glu	Glu	Glu	Ser	Lys	Ile	Glu	Arg	
			500					505					510			
Gln	Lys	Val	Asn	Gly	Val	Lys	Leu	Glu	Glu	Asn	Ser	Thr	Tyr	Lys	Ile	
		515					520					525				
Leu	Ser	Ile	Tyr	Ser	Ser	Val	Ala	Ser	Ser	Leu	Val	Leu	Leu	Leu	Met	
	530					535					540					
Ile	Ile	Gly	Gly	Phe	Ile	Phe	Gly	Cys	Gln	Asn	Gly	Asn	Val	Arg	Cys	
545					550					555					560	
Thr	Phe	Cys	Ile													
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1				5				10						15		
His	Ala	Asp	Arg	Ile	Cys	Val	Gly	Tyr	Leu	Ser	Thr	Asn	Ser	Ser	Glu	
		20						25					30			
Arg	Val	Asp	Thr	Leu	Leu	Glu	Asn	Gly	Val	Pro	Val	Thr	Ser	Ser	Ile	
		35					40					45				
Asp	Leu	Ile	Glu	Thr	Asn	His	Thr	Gly	Thr	Tyr	Cys	Ser	Leu	Asn	Gly	
	50					55					60					
Val	Ser	Pro	Val	His	Leu	Gly	Asp	Cys	Ser	Phe	Glu	Gly	Trp	Ile	Val	
65					70					75					80	
Gly	Asn	Pro	Ala	Cys	Thr	Ser	Asn	Phe	Gly	Ile	Arg	Glu	Trp	Ser	Tyr	
			85						90					95		
Leu	Ile	Glu	Asp	Pro	Ala	Ala	Pro	His	Gly	Leu	Cys	Tyr	Pro	Gly	Glu	
		100						105					110			
Leu	Asn	Asn	Asn	Gly	Glu	Leu	Arg	His	Leu	Phe	Ser	Gly	Ile	Arg	Ser	
	115						120					125				
Phe	Ser	Arg	Thr	Glu	Leu	Ile	Pro	Pro	Thr	Ser	Trp	Gly	Glu	Val	Leu	

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130					135					140					
Asp 145	Gly	Thr	Thr	Ser	Ala 150	Cys	Arg	Asp	Asn	Thr 155	Gly	Thr	Asn	Ser	Phe 160
Tyr	Arg	Asn	Leu	Val 165	Trp	Phe	Ile	Lys	Lys 170	Asn	Asn	Arg	Tyr	Pro	Val 175
Ile	Ser	Lys	Thr 180	Tyr	Asn	Asn	Thr	Thr 185	Gly	Arg	Asp	Val	Leu 190	Val	Leu
Trp	Gly	Ile 195	His	His	Pro	Val	Ser 200	Val	Asp	Glu	Thr	Lys 205	Thr	Leu	Tyr
Val	Asn 210	Ser	Asp	Pro	Tyr	Thr 215	Leu	Val	Ser	Thr	Lys 220	Ser	Trp	Ser	Glu
Lys 225	Tyr	Lys	Leu	Glu	Thr 230	Gly	Val	Arg	Pro	Gly 235	Tyr	Asn	Gly	Gln	Arg 240
Ser	Trp	Met	Lys 245	Ile	Tyr	Trp	Ser	Leu	Ile 250	His	Pro	Gly	Glu	Met	Ile 255
Thr	Phe	Glu	Ser 260	Asn	Gly	Gly	Phe	Leu	Ala 265	Pro	Arg	Tyr	Gly	Tyr	Ile 270
Ile	Glu	Glu 275	Tyr	Gly	Lys	Gly	Arg 280	Ile	Phe	Gln	Ser	Arg 285	Ile	Arg	Met
Ser	Arg 290	Cys	Asn	Thr	Lys	Cys 295	Gln	Thr	Ser	Val	Gly 300	Gly	Ile	Asn	Thr
Asn 305	Arg	Thr	Phe	Gln	Asn 310	Ile	Asp	Lys	Asn	Ala 315	Leu	Gly	Asp	Cys	Pro 320
Lys	Tyr	Ile	Lys 325	Ser	Gly	Gln	Leu	Lys	Leu 330	Ala	Thr	Gly	Leu	Arg	Asn 335
Val	Pro	Ala	Ile 340	Ser	Asn	Arg	Gly	Leu	Phe 345	Gly	Ala	Ile	Ala	Gly	Phe 350
Ile	Glu	Gly 355	Gly	Trp	Pro	Gly	Leu	Ile	Asn	Gly	Trp	Tyr 365	Gly	Phe	Gln
His 370	Gln	Asn	Glu	Gln	Gly	Thr 375	Gly	Ile	Ala	Ala	Asp 380	Lys	Glu	Ser	Thr
Gln 385	Lys	Ala	Ile	Asp	Gln 390	Ile	Thr	Thr	Lys	Ile 395	Asn	Asn	Ile	Ile	Asp 400
Lys	Met	Asn	Gly	Asn 405	Tyr	Asp	Ser	Ile	Arg 410	Gly	Glu	Phe	Asn	Gln	Val 415
Glu	Lys	Arg	Ile 420	Asn	Met	Leu	Ala	Asp 425	Arg	Ile	Asp	Asp	Ala	Val	Thr 430
Asp	Ile 435	Trp	Ser	Tyr	Asn	Ala 440	Lys	Leu	Leu	Val	Leu 445	Leu	Glu	Asn	Asp
Lys	Thr 450	Leu	Asp	Met	His	Asp 455	Ala	Asn	Val	Lys	Asn 460	Leu	His	Glu	Gln
Val 465	Arg	Arg	Glu	Leu	Lys 470	Asp	Asn	Ala	Ile	Asp 475	Glu	Gly	Asn	Gly	Cys 480
Phe	Glu	Leu	Leu 485	His	Lys	Cys	Asn	Asp 490	Ser	Cys	Met	Glu	Thr	Ile	Arg 495
Asn	Gly	Thr 500	Tyr	Asp	His	Thr	Glu 505	Tyr	Ala	Glu	Glu	Ser	Lys 510	Leu	Lys
Arg	Gln	Glu 515	Ile	Asp	Gly	Ile	Lys 520	Leu	Lys	Ser	Glu	Asp 525	Asn	Val	Tyr
Lys	Ala 530	Leu	Ser	Ile	Tyr	Ser 535	Cys	Ile	Ala	Ser	Ser 540	Val	Val	Leu	Val

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Gly	Leu	Ile	Leu	Ser	Phe	Ile	Met	Trp	Ala	Cys	Ser	Ser	Gly	Asn	Cys
545					550					555					560
Arg	Phe	Asn	Val	Cys	Ile										
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1				5					10					15	
Ser	Gln	Ile	Thr	Asn	Gly	Thr	Thr	Gly	Asn	Pro	Ile	Ile	Cys	Leu	Gly
			20					25					30		
His	His	Ala	Val	Glu	Asn	Gly	Thr	Ser	Val	Lys	Thr	Leu	Thr	Asp	Asn
		35					40					45			
His	Val	Glu	Val	Val	Ser	Ala	Lys	Glu	Leu	Val	Glu	Thr	Asn	His	Thr
	50					55					60				
Asp	Glu	Leu	Cys	Pro	Ser	Pro	Leu	Lys	Leu	Val	Asp	Gly	Gln	Asp	Cys
65					70					75					80
His	Leu	Ile	Asn	Gly	Ala	Leu	Gly	Ser	Pro	Gly	Cys	Asp	Arg	Leu	Gln
			85						90					95	
Asp	Thr	Thr	Trp	Asp	Val	Phe	Ile	Glu	Arg	Pro	Thr	Ala	Val	Asp	Thr
			100					105					110		
Cys	Tyr	Pro	Phe	Asp	Val	Pro	Asp	Tyr	Gln	Ser	Leu	Arg	Ser	Ile	Leu
		115					120					125			
Ala	Ser	Ser	Gly	Ser	Leu	Glu	Phe	Ile	Ala	Glu	Gln	Phe	Thr	Trp	Asn
	130					135					140				
Gly	Val	Lys	Val	Asp	Gly	Ser	Ser	Ser	Ala	Cys	Leu	Arg	Gly	Gly	Arg
145					150					155					160
Asn	Ser	Phe	Phe	Ser	Arg	Leu	Asn	Trp	Leu	Thr	Lys	Ala	Thr	Asn	Gly
				165					170					175	
Asn	Tyr	Gly	Pro	Ile	Asn	Val	Thr	Lys	Glu	Asn	Thr	Gly	Ser	Tyr	Val
		180						185					190		
Arg	Leu	Tyr	Leu	Trp	Gly	Val	His	His	Pro	Ser	Ser	Asp	Asn	Glu	Gln
		195					200					205			
Thr	Asp	Leu	Tyr	Lys	Val	Ala	Thr	Gly	Arg	Val	Thr	Val	Ser	Thr	Arg
	210					215					220				
Ser	Asp	Gln	Ile	Ser	Ile	Val	Pro	Asn	Ile	Gly	Ser	Arg	Pro	Arg	Val
225					230					235					240
Arg	Asn	Gln	Ser	Gly	Arg	Ile	Ser	Ile	Tyr	Trp	Thr	Leu	Val	Asn	Pro
				245					250					255	
Gly	Asp	Ser	Ile	Ile	Phe	Asn	Ser	Ile	Gly	Asn	Leu	Ile	Ala	Pro	Arg
			260					265					270		
Gly	His	Tyr	Lys	Ile	Ser	Lys	Ser	Thr	Lys	Ser	Thr	Val	Leu	Lys	Ser
		275					280					285			
Asp	Lys	Arg	Ile	Gly	Ser	Cys	Thr	Ser	Pro	Cys	Leu	Thr	Asp	Lys	Gly
	290					295					300				

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Ser	Ile	Gln	Ser	Asp	Lys	Pro	Phe	Gln	Asn	Val	Ser	Arg	Ile	Ala	Ile	
305					310					315					320	
Gly	Asn	Cys	Pro	Lys	Tyr	Val	Lys	Gln	Gly	Ser	Leu	Met	Leu	Ala	Thr	
				325					330					335		
Gly	Met	Arg	Asn	Ile	Pro	Gly	Lys	Gln	Ala	Lys	Gly	Leu	Phe	Gly	Ala	
			340					345					350			
Ile	Ala	Gly	Phe	Ile	Glu	Asn	Gly	Trp	Gln	Gly	Leu	Ile	Asp	Gly	Trp	
		355					360					365				
Tyr	Gly	Phe	Arg	His	Gln	Asn	Ala	Glu	Gly	Thr	Gly	Thr	Ala	Ala	Asp	
	370					375					380					
Leu	Lys	Ser	Thr	Gln	Ala	Ala	Ile	Asp	Gln	Ile	Asn	Gly	Lys	Leu	Asn	
385					390					395					400	
Arg	Leu	Ile	Glu	Lys	Thr	Asn	Glu	Lys	Tyr	His	Gln	Ile	Glu	Lys	Glu	
				405					410					415		
Phe	Glu	Gln	Val	Glu	Gly	Arg	Ile	Gln	Asp	Leu	Glu	Lys	Tyr	Val	Glu	
			420					425					430			
Asp	Thr	Lys	Ile	Asp	Leu	Trp	Ser	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Ala	
		435					440					445				
Leu	Glu	Asn	Gln	His	Thr	Ile	Asp	Val	Thr	Asp	Ser	Glu	Met	Asn	Lys	
	450					455					460					
Leu	Phe	Glu	Arg	Val	Arg	Arg	Gln	Leu	Arg	Glu	Asn	Ala	Glu	Asp	Gln	
465					470				475						480	
Gly	Asn	Gly	Cys	Phe	Glu	Ile	Phe	His	Gln	Cys	Asp	Asn	Asn	Cys	Ile	
				485					490					495		
Glu	Ser	Ile	Arg	Asn	Gly	Thr	Tyr	Asp	His	Asn	Ile	Tyr	Arg	Asp	Glu	
			500					505					510			
Ala	Ile	Asn	Asn	Arg	Ile	Lys	Ile	Asn	Pro	Val	Thr	Leu	Thr	Met	Gly	
		515					520					525				
Tyr	Lys	Asp	Ile	Ile	Leu	Trp	Ile	Ser	Phe	Ser	Met	Ser	Cys	Phe	Val	
	530					535					540					
Phe	Val	Ala	Leu	Ile	Leu	Gly	Phe	Val	Leu	Trp	Ala	Cys	Gln	Asn	Gly	
545					550				555						560	
Asn	Ile	Arg	Cys	Gln	Ile	Cys	Ile									
				565												
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<211> LENGTH: 570																
<212> TYPE: PRT																
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<220> FEATURE:																
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<223> OTHER INFORMATION: HA Type 15																
<400> SEQUENCE: 15																
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1				5				10					15			
Lys	Ser	Asp	Lys	Ile	Cys	Leu	Gly	His	His	Ala	Val	Ala	Asn	Gly	Thr	
			20					25					30			
Lys	Val	Asn	Thr	Leu	Thr	Glu	Arg	Gly	Val	Glu	Val	Val	Asn	Ala	Thr	
		35				40						45				
Glu	Thr	Val	Glu	Ile	Thr	Gly	Ile	Asp	Lys	Val	Cys	Thr	Lys	Gly	Lys	
	50					55					60					
Lys	Ala	Val	Asp	Leu	Gly	Ser	Cys	Gly	Ile	Leu	Gly	Thr	Ile	Ile	Gly	

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65					70					75					80
Pro	Pro	Gln	Cys	Asp	Leu	His	Leu	Glu	Phe	Lys	Ala	Asp	Leu	Ile	Ile
			85						90					95	
Glu	Arg	Arg	Asn	Ser	Ser	Asp	Ile	Cys	Tyr	Pro	Gly	Arg	Phe	Thr	Asn
			100					105					110		
Glu	Glu	Ala	Leu	Arg	Gln	Ile	Ile	Arg	Glu	Ser	Gly	Gly	Ile	Asp	Lys
		115					120					125			
Glu	Ser	Met	Gly	Phe	Arg	Tyr	Ser	Gly	Ile	Arg	Thr	Asp	Gly	Ala	Thr
	130					135					140				
Ser	Ala	Cys	Lys	Arg	Thr	Val	Ser	Ser	Phe	Tyr	Ser	Glu	Met	Lys	Trp
145					150					155					160
Leu	Ser	Ser	Ser	Met	Asn	Asn	Gln	Val	Phe	Pro	Gln	Leu	Asn	Gln	Thr
				165					170					175	
Tyr	Arg	Asn	Thr	Arg	Lys	Glu	Pro	Ala	Leu	Ile	Val	Trp	Gly	Val	His
		180						185					190		
His	Ser	Ser	Ser	Leu	Asp	Glu	Gln	Asn	Lys	Leu	Tyr	Gly	Thr	Gly	Asn
	195						200					205			
Lys	Leu	Ile	Thr	Val	Gly	Ser	Ser	Lys	Tyr	Gln	Gln	Ser	Phe	Ser	Pro
	210					215					220				
Ser	Pro	Gly	Ala	Arg	Pro	Lys	Val	Asn	Gly	Gln	Ala	Gly	Arg	Ile	Asp
225					230					235					240
Phe	His	Trp	Met	Leu	Leu	Asp	Pro	Gly	Asp	Thr	Val	Thr	Phe	Thr	Phe
			245						250					255	
Asn	Gly	Ala	Phe	Ile	Ala	Pro	Asp	Arg	Ala	Thr	Phe	Leu	Arg	Ser	Asn
		260						265					270		
Ala	Pro	Ser	Gly	Ile	Glu	Tyr	Asn	Gly	Lys	Ser	Leu	Gly	Ile	Gln	Ser
		275					280					285			
Asp	Ala	Gln	Ile	Asp	Glu	Ser	Cys	Glu	Gly	Glu	Cys	Phe	Tyr	Ser	Gly
	290					295					300				
Gly	Thr	Ile	Asn	Ser	Pro	Leu	Pro	Phe	Gln	Asn	Ile	Asp	Ser	Arg	Ala
305					310					315					320
Val	Gly	Lys	Cys	Pro	Arg	Tyr	Val	Lys	Gln	Ser	Ser	Leu	Pro	Leu	Ala
			325						330					335	
Leu	Gly	Met	Lys	Asn	Val	Pro	Glu	Lys	Ile	Arg	Thr	Arg	Gly	Leu	Phe
		340						345					350		
Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Asn	Gly	Trp	Glu	Gly	Leu	Ile	Asp
		355					360					365			
Gly	Trp	Tyr	Gly	Phe	Arg	His	Gln	Asn	Ala	Gln	Gly	Gln	Gly	Thr	Ala
	370					375					380				
Ala	Asp	Tyr	Lys	Ser	Thr	Gln	Ala	Ala	Ile	Asp	Gln	Ile	Thr	Gly	Lys
385					390					395					400
Leu	Asn	Arg	Leu	Ile	Glu	Lys	Thr	Asn	Lys	Gln	Phe	Glu	Leu	Ile	Asp
			405						410					415	
Asn	Glu	Phe	Thr	Glu	Val	Glu	Gln	Gln	Ile	Gly	Asn	Val	Ile	Asn	Trp
			420					425					430		
Thr	Arg	Asp	Ser	Leu	Thr	Glu	Ile	Trp	Ser	Tyr	Asn	Ala	Glu	Leu	Leu
		435					440					445			
Val	Ala	Met	Glu	Asn	Gln	His	Thr	Ile	Asp	Leu	Ala	Asp	Ser	Glu	Met
	450					455					460				
Asn	Lys	Leu	Tyr	Glu	Arg	Val	Arg	Arg	Gln	Leu	Arg	Glu	Asn	Ala	Glu
465					470					475					480

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Glu	Asp	Gly	Thr	Gly	Cys	Phe	Glu	Ile	Phe	His	Arg	Cys	Asp	Asp	Gln
				485					490					495	
Cys	Met	Glu	Ser	Ile	Arg	Asn	Asn	Thr	Tyr	Asn	His	Thr	Glu	Tyr	Arg
			500					505					510		
Gln	Glu	Ala	Leu	Gln	Asn	Arg	Ile	Met	Ile	Asn	Pro	Val	Lys	Leu	Ser
		515					520					525			
Ser	Gly	Tyr	Lys	Asp	Val	Ile	Leu	Trp	Phe	Ser	Phe	Gly	Ala	Ser	Cys
	530					535					540				
Val	Met	Leu	Leu	Ala	Ile	Ala	Met	Gly	Leu	Ile	Phe	Met	Cys	Val	Lys
545					550					555					560
Asn	Gly	Asn	Leu	Arg	Cys	Thr	Ile	Cys	Ile						
				565					570						
<210> SEQ ID NO 16															
<211> LENGTH: 564															
<212> TYPE: PRT															
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<221> NAME/KEY: MISC_FEATURE															
<222> LOCATION: (1)..(564)															
<223> OTHER INFORMATION: HA Type 16															
<400> SEQUENCE: 16															
Met	Ala	Lys	Thr	Leu	Tyr	Leu	Leu	Val	Leu	Ile	Phe	Val	Lys	Tyr	Ser
1				5					10					15	
Arg	Ala	Asp	Lys	Ile	Cys	Ile	Gly	Tyr	Leu	Ser	Asn	Asn	Ser	Thr	Asp
			20					25					30		
Thr	Val	Asp	Thr	Leu	Thr	Glu	Asn	Gly	Val	Pro	Val	Thr	Ser	Ser	Ile
		35					40					45			
Asp	Leu	Val	Glu	Thr	Asn	His	Thr	Gly	Thr	Tyr	Cys	Ser	Leu	Asn	Gly
	50					55					60				
Val	Ser	Pro	Ile	His	Leu	Gly	Asp	Cys	Ser	Phe	Glu	Gly	Trp	Ile	Val
65					70					75					80
Gly	Asn	Pro	Ser	Cys	Ala	Ser	Asn	Ile	Asn	Ile	Arg	Glu	Trp	Ser	Tyr
				85					90					95	
Leu	Ile	Glu	Asp	Pro	Asn	Ala	Pro	His	Lys	Leu	Cys	Phe	Pro	Gly	Glu
		100						105					110		
Val	Asp	Asn	Asn	Gly	Glu	Leu	Arg	His	Leu	Phe	Ser	Gly	Val	Asn	Ser
		115					120					125			
Phe	Ser	Arg	Thr	Glu	Leu	Ile	Pro	Pro	Ser	Lys	Trp	Gly	Asp	Ile	Leu
	130					135						140			
Glu	Gly	Thr	Thr	Ala	Ser	Cys	Gln	Asn	Arg	Gly	Ala	Asn	Ser	Phe	Tyr
145				150						155					160
Arg	Asn	Leu	Ile	Trp	Leu	Val	Asn	Lys	Leu	Asn	Lys	Tyr	Pro	Val	Val
			165						170					175	
Lys	Gly	Glu	Tyr	Asn	Asn	Thr	Thr	Gly	Arg	Asp	Val	Leu	Val	Leu	Trp
		180						185					190		
Gly	Ile	His	His	Pro	Asp	Thr	Glu	Ala	Thr	Ala	Asn	Lys	Leu	Tyr	Val
		195					200					205			
Asn	Lys	Asn	Pro	Tyr	Thr	Leu	Val	Ser	Thr	Lys	Glu	Trp	Ser	Arg	Arg
	210					215					220				
Tyr	Glu	Leu	Glu	Ile	Gly	Thr	Arg	Ile	Gly	Asp	Gly	Gln	Arg	Ser	Trp
225				230						235					240

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Met	Lys	Ile	Tyr	Trp	His	Leu	Met	His	Pro	Gly	Glu	Arg	Ile	Thr	Phe	
				245					250					255		
Glu	Ser	Ser	Gly	Gly	Leu	Leu	Ala	Pro	Arg	Tyr	Gly	Tyr	Ile	Ile	Glu	
			260					265					270			
Lys	Tyr	Gly	Thr	Gly	Arg	Ile	Phe	Gln	Ser	Gly	Val	Arg	Leu	Ala	Lys	
		275					280					285				
Cys	Asn	Thr	Lys	Cys	Gln	Thr	Ser	Met	Gly	Gly	Ile	Asn	Thr	Asn	Lys	
	290					295					300					
Thr	Phe	Gln	Asn	Ile	Glu	Arg	Asn	Ala	Leu	Gly	Asp	Cys	Pro	Lys	Tyr	
305					310					315					320	
Ile	Lys	Ser	Gly	Gln	Leu	Lys	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Val	Pro	
				325					330					335		
Ser	Ile	Val	Glu	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	
			340					345					350			
Gly	Gly	Trp	Pro	Gly	Leu	Ile	Asn	Gly	Trp	Tyr	Gly	Phe	Gln	His	Gln	
		355					360					365				
Asn	Glu	Gln	Gly	Thr	Gly	Ile	Ala	Ala	Asp	Lys	Thr	Ser	Thr	Gln	Lys	
	370					375					380					
Ala	Ile	Asn	Glu	Ile	Thr	Thr	Lys	Ile	Asn	Asn	Ile	Ile	Glu	Lys	Met	
385					390					395					400	
Asn	Gly	Asn	Tyr	Asp	Ser	Ile	Arg	Gly	Glu	Phe	Asn	Gln	Val	Glu	Lys	
			405						410				415			
Arg	Ile	Asn	Met	Ile	Ala	Asp	Arg	Val	Asp	Asp	Ala	Val	Thr	Asp	Ile	
		420						425					430			
Trp	Ser	Tyr	Asn	Ala	Lys	Leu	Leu	Val	Leu	Ile	Glu	Asn	Asp	Arg	Thr	
		435				440						445				
Leu	Asp	Leu	His	Asp	Ala	Asn	Val	Arg	Asn	Leu	His	Glu	Gln	Ile	Lys	
	450					455					460					
Arg	Ala	Leu	Lys	Asp	Asn	Ala	Ile	Asp	Glu	Gly	Asp	Gly	Cys	Phe	Ser	
465					470					475					480	
Ile	Leu	His	Lys	Cys	Asn	Asp	Ser	Cys	Met	Glu	Thr	Ile	Arg	Asn	Gly	
			485						490				495			
Thr	Tyr	Asn	His	Glu	Asp	Tyr	Lys	Glu	Glu	Ser	Gln	Leu	Lys	Arg	Gln	
		500						505					510			
Glu	Ile	Glu	Gly	Ile	Lys	Leu	Lys	Thr	Glu	Asp	Asn	Val	Tyr	Lys	Ile	
		515					520					525				
Leu	Ser	Ile	Tyr	Ser	Cys	Ile	Ala	Ser	Ser	Val	Val	Leu	Val	Gly	Leu	
	530					535					540					
Ile	Leu	Ala	Phe	Ile	Leu	Trp	Ala	Cys	Ser	Ser	Gly	Asn	Cys	Arg	Phe	
545					550					555					560	
Asn	Val	Cys	Ile													

<210> SEQ ID NO 17
<211> LENGTH: 469
<212> TYPE: PRT
<213> ORGANISM: Influenza A virus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(469)
<223> OTHER INFORMATION: NA Type 1

<400> SEQUENCE: 17

Met	Asn	Pro	Asn	Gln	Lys	Ile	Ile	Thr	Ile	Gly	Ser	Ile	Cys	Met	Val	
1				5				10					15			

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Val	Gly	Ile	Ile	Ser	Leu	Ile	Leu	Gln	Ile	Gly	Asn	Ile	Ile	Ser	Ile	
			20					25					30			
Trp	Val	Ser	His	Ser	Ile	Gln	Thr	Gly	Asn	Gln	Asn	His	Pro	Glu	Thr	
		35					40					45				
Cys	Asn	Gln	Ser	Ile	Ile	Thr	Tyr	Glu	Asn	Asn	Thr	Trp	Val	Asn	Gln	
	50					55					60					
Thr	Tyr	Val	Asn	Ile	Ser	Asn	Thr	Asn	Val	Val	Ala	Gly	Gln	Asp	Ala	
65					70					75					80	
Thr	Ser	Val	Ile	Leu	Thr	Gly	Asn	Ser	Ser	Leu	Cys	Pro	Ile	Ser	Gly	
				85					90					95		
Trp	Ala	Ile	Tyr	Ser	Lys	Asp	Asn	Gly	Ile	Arg	Ile	Gly	Ser	Lys	Gly	
			100					105					110			
Asp	Val	Phe	Val	Ile	Arg	Glu	Pro	Phe	Ile	Ser	Cys	Ser	His	Leu	Glu	
		115					120					125				
Cys	Arg	Thr	Phe	Phe	Leu	Thr	Gln	Gly	Ala	Leu	Leu	Asn	Asp	Lys	His	
	130					135						140				
Ser	Asn	Gly	Thr	Val	Lys	Asp	Arg	Ser	Pro	Tyr	Arg	Thr	Leu	Met	Ser	
145					150					155					160	
Cys	Pro	Val	Gly	Glu	Ala	Pro	Ser	Pro	Tyr	Asn	Ser	Arg	Phe	Glu	Ser	
				165					170					175		
Val	Ala	Trp	Ser	Ala	Ser	Ala	Cys	His	Asp	Gly	Met	Gly	Trp	Leu	Thr	
			180					185					190			
Ile	Gly	Ile	Ser	Gly	Pro	Asp	Asn	Gly	Ala	Val	Ala	Val	Leu	Lys	Tyr	
		195					200						205			
Asn	Gly	Ile	Ile	Thr	Asp	Thr	Ile	Lys	Ser	Trp	Arg	Asn	Asn	Ile	Leu	
	210					215					220					
Arg	Thr	Gln	Glu	Ser	Glu	Cys	Ala	Cys	Val	Asn	Gly	Ser	Cys	Phe	Thr	
225					230					235					240	
Ile	Met	Thr	Asp	Gly	Pro	Ser	Asn	Gly	Gln	Ala	Ser	Tyr	Lys	Ile	Leu	
				245					250					255		
Lys	Ile	Glu	Lys	Gly	Lys	Val	Thr	Lys	Ser	Ile	Glu	Leu	Asn	Ala	Pro	
			260					265					270			
Asn	Tyr	His	Tyr	Glu	Glu	Cys	Ser	Cys	Tyr	Pro	Asp	Thr	Gly	Lys	Val	
		275					280					285				
Met	Cys	Val	Cys	Arg	Asp	Asn	Trp	His	Gly	Ser	Asn	Arg	Pro	Trp	Val	
	290					295					300					
Ser	Phe	Asp	Gln	Asn	Leu	Asp	Tyr	Gln	Ile	Gly	Tyr	Ile	Cys	Ser	Gly	
305					310					315					320	
Val	Phe	Gly	Asp	Asn	Pro	Arg	Pro	Asn	Asp	Gly	Thr	Gly	Ser	Cys	Gly	
				325					330					335		
Pro	Val	Ser	Ser	Asn	Gly	Ala	Asn	Gly	Ile	Lys	Gly	Phe	Ser	Phe	Arg	
			340					345					350			
Tyr	Asp	Asn	Gly	Val	Trp	Ile	Gly	Arg	Thr	Lys	Ser	Thr	Ser	Ser	Arg	
		355					360						365			
Ser	Gly	Phe	Glu	Met	Ile	Trp	Asp	Pro	Asn	Gly	Trp	Thr	Glu	Thr	Asp	
	370					375					380					
Ser	Ser	Phe	Ser	Val	Arg	Gln	Asp	Ile	Val	Ala	Ile	Thr	Asp	Trp	Ser	
385					390					395					400	
Gly	Tyr	Ser	Gly	Ser	Phe	Val	Gln	His	Pro	Glu	Leu	Thr	Gly	Leu	Asp	
				405					410					415		

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Cys	Met	Arg	Pro	Cys	Phe	Trp	Val	Glu	Leu	Ile	Arg	Gly	Gln	Pro	Lys	
			420					425					430			
Glu	Asn	Thr	Ile	Trp	Thr	Ser	Gly	Ser	Ser	Ile	Ser	Phe	Cys	Gly	Val	
		435					440					445				
Asn	Ser	Asp	Thr	Val	Gly	Trp	Ser	Trp	Pro	Asp	Gly	Ala	Glu	Leu	Pro	
	450					455					460					
Phe	Ser	Ile	Asp	Lys												
465																
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<212> TYPE: PRT																
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<220> FEATURE:																
<221> NAME/KEY: MISC_FEATURE																
<222> LOCATION: (1)..(451)																
<223> OTHER INFORMATION: NA Type 2																
<400> SEQUENCE: 18																
Met	Asn	Pro	Asn	Gln	Lys	Ile	Ile	Thr	Ile	Gly	Ser	Val	Ser	Leu	Thr	
1				5					10					15		
Ile	Ala	Thr	Val	Cys	Phe	Leu	Met	Gln	Ile	Ala	Ile	Leu	Ala	Thr	Thr	
			20					25					30			
Val	Thr	Leu	His	Phe	Lys	Gln	Asn	Glu	Cys	Ser	Ile	Pro	Ala	Lys	Asn	
		35					40					45				
Gln	Val	Val	Pro	Cys	Glu	Pro	Thr	Ile	Ala	Glu	Arg	Pro	Lys	Ala	Val	
	50					55					60					
Asp	Tyr	Arg	Ile	Trp	Ser	Lys	Pro	Gln	Cys	Gln	Ile	Thr	Gly	Phe	Ala	
65					70				75						80	
Pro	Phe	Ser	Lys	Asp	Asn	Ser	Ile	Arg	Leu	Ser	Ala	Gly	Gly	Asp	Ile	
			85						90					95		
Trp	Val	Thr	Arg	Glu	Pro	Tyr	Val	Ser	Cys	Glu	Thr	Ser	Lys	Cys	Tyr	
			100					105					110			
Gln	Phe	Ala	Leu	Gly	Gln	Gly	Thr	Thr	Leu	Asp	Asn	Lys	His	Ser	Asn	
		115					120					125				
Gly	Thr	Ile	His	Asp	Arg	Ile	Pro	His	Arg	Thr	Leu	Leu	Met	Ser	Glu	
	130					135					140					
Leu	Gly	Val	Pro	Phe	His	Leu	Gly	Thr	Lys	Gln	Val	Cys	Ile	Ala	Trp	
145					150					155					160	
Ser	Ser	Ser	Ser	Cys	His	Asp	Gly	Lys	Ala	Trp	Leu	His	Val	Cys	Val	
				165					170					175		
Thr	Gly	Asp	Asp	Arg	Asn	Ala	Thr	Ala	Ser	Phe	Ile	Tyr	Asp	Gly	Met	
		180						185					190			
Leu	Val	Asp	Ser	Ile	Ser	Ser	Trp	Ser	Gln	Asn	Ile	Leu	Arg	Thr	Gln	
	195						200					205				
Glu	Ser	Glu	Cys	Val	Cys	Ile	Asn	Gly	Thr	Cys	Thr	Val	Val	Met	Thr	
	210					215					220					
Asp	Gly	Ser	Ala	Ser	Gly	Lys	Ala	Asp	Thr	Arg	Ile	Leu	Phe	Ile	Lys	
225					230					235					240	
Glu	Gly	Lys	Ile	Ala	His	Ile	Ser	Pro	Leu	Ser	Gly	Ser	Ala	Gln	His	
			245						250					255		
Ile	Glu	Glu	Cys	Ser	Cys	Tyr	Pro	Gln	Tyr	Ser	Asn	Val	Arg	Cys	Val	
		260						265					270			
Cys	Arg	Asp	Asn	Trp	Lys	Gly	Ser	Asn	Arg	Pro	Ile	Ile	Asp	Ile	Asn	

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275					280					285									
Met	Ala	Asp	Tyr	Ser	Ile	Asp	Ser	Ser	Tyr	Val	Cys	Ser	Gly	Leu	Val				
	290					295					300								
Gly	Asp	Thr	Pro	Arg	Asn	Asp	Asp	Ser	Ser	Ser	Ser	Ser	Asn	Cys	Arg				
305					310					315					320				
Asp	Pro	Asn	Asn	Glu	Arg	Gly	Asn	Pro	Gly	Val	Lys	Gly	Trp	Ala	Phe				
				325					330					335					
Asp	Asp	Gly	Asn	Asp	Val	Trp	Met	Gly	Arg	Thr	Ile	Ser	Lys	Asp	Ser				
			340					345					350						
Arg	Ser	Gly	Tyr	Glu	Thr	Phe	Lys	Val	Ile	Asp	Gly	Trp	Ala	Thr	Ala				
	355					360				365									
Asn	Ser	Lys	Ser	Gln	Thr	Asn	Arg	Gln	Val	Ile	Val	Asp	Asn	Asn	Asn				
	370					375					380								
Trp	Ser	Gly	Tyr	Ser	Gly	Ile	Phe	Ser	Val	Glu	Asn	Lys	Gly	Cys	Ile				
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			405						410					415					
Arg	Val	Trp	Trp	Thr	Ser	Asn	Ser	Ile	Val	Val	Phe	Cys	Gly	Thr	Ser				
			420					425					430						
Gly	Thr	Tyr	Gly	Thr	Gly	Ser	Trp	Pro	Asp	Gly	Ala	Asn	Ile	Asp	Phe				
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Leu	Ser	Thr	Ile	Ala	Leu	Leu	Ile	Gly	Val	Gly	Asn	Leu	Ile	Phe	Asn				
			20					25					30						
Thr	Val	Ile	His	Glu	Lys	Ile	Gly	Asp	His	Gln	Thr	Val	Val	Tyr	Pro				
		35					40					45							
Thr	Ile	Thr	Ala	Pro	Val	Val	Pro	Asn	Cys	Ser	Asp	Thr	Ile	Ile	Thr				
	50					55					60								
Tyr	Asn	Asn	Thr	Val	Ile	Asn	Asn	Ile	Thr	Thr	Thr	Ile	Ile	Thr	Glu				
65				70						75					80				
Ala	Glu	Arg	His	Phe	Lys	Pro	Ser	Leu	Pro	Leu	Cys	Pro	Phe	Arg	Gly				
			85					90						95					
Phe	Phe	Pro	Phe	His	Lys	Asp	Asn	Ala	Ile	Arg	Leu	Gly	Glu	Asn	Lys				
		100						105					110						
Asp	Val	Ile	Val	Thr	Arg	Glu	Pro	Tyr	Val	Ser	Cys	Asp	Asn	Asp	Asn				
		115					120					125							
Cys	Trp	Ser	Phe	Ala	Leu	Ala	Gln	Gly	Ala	Leu	Leu	Gly	Thr	Lys	His				
	130					135					140								
Ser	Asn	Gly	Thr	Ile	Lys	Asp	Arg	Thr	Pro	Tyr	Arg	Ser	Leu	Ile	Arg				
145					150					155					160				

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Phe	Pro	Ile	Gly	Thr	Ala	Pro	Val	Leu	Gly	Asn	Tyr	Lys	Glu	Ile	Cys	
				165					170					175		
Val	Ala	Trp	Ser	Ser	Ser	Ser	Cys	Phe	Asp	Gly	Lys	Glu	Trp	Met	His	
			180					185					190			
Val	Cys	Met	Thr	Gly	Asn	Asp	Asn	Asp	Ala	Ser	Ala	Gln	Ile	Ile	Tyr	
		195					200					205				
Ala	Gly	Lys	Met	Thr	Asp	Ser	Ile	Lys	Ser	Trp	Arg	Arg	Asp	Ile	Leu	
	210					215				220						
Arg	Thr	Gln	Glu	Ser	Glu	Cys	Gln	Cys	Ile	Asp	Gly	Thr	Cys	Val	Val	
225					230					235					240	
Ala	Val	Thr	Asp	Gly	Pro	Ala	Ala	Asn	Ser	Ala	Asp	His	Arg	Val	Tyr	
				245					250					255		
Trp	Ile	Arg	Glu	Gly	Lys	Val	Ile	Lys	Tyr	Glu	Asn	Val	Pro	Lys	Thr	
			260					265					270			
Lys	Ile	Gln	His	Leu	Glu	Glu	Cys	Ser	Cys	Tyr	Val	Asp	Thr	Asp	Val	
		275					280					285				
Tyr	Cys	Val	Cys	Arg	Asp	Asn	Trp	Lys	Gly	Ser	Asn	Arg	Pro	Trp	Met	
	290					295					300					
Arg	Ile	Asn	Asn	Glu	Thr	Ile	Leu	Glu	Thr	Gly	Tyr	Val	Cys	Ser	Lys	
305					310					315					320	
Phe	His	Ser	Asp	Thr	Pro	Arg	Pro	Ala	Asp	Pro	Ser	Thr	Val	Ser	Cys	
				325					330					335		
Asp	Ser	Pro	Ser	Asn	Val	Asn	Gly	Gly	Pro	Gly	Val	Lys	Gly	Phe	Gly	
			340					345					350			
Phe	Lys	Thr	Gly	Asp	Asp	Val	Trp	Leu	Gly	Arg	Thr	Val	Ser	Thr	Asn	
		355					360					365				
Gly	Arg	Ser	Gly	Phe	Glu	Ile	Ile	Lys	Val	Thr	Glu	Gly	Trp	Ile	Asn	
	370					375					380					
Ser	Pro	Asn	His	Ala	Lys	Ser	Val	Thr	Gln	Thr	Leu	Val	Ser	Asn	Asn	
385					390					395					400	
Asp	Trp	Ser	Gly	Tyr	Ser	Gly	Ser	Phe	Ile	Val	Glu	Asn	Asn	Gly	Cys	
			405						410					415		
Phe	Gln	Pro	Cys	Phe	Tyr	Ile	Glu	Leu	Ile	Arg	Gly	Arg	Thr	Asn	Lys	
			420					425					430			
Asn	Asp	Asp	Val	Ser	Trp	Thr	Ser	Asn	Ser	Ile	Val	Thr	Phe	Cys	Gly	
		435					440					445				
Leu	Asp	Asn	Glu	Pro	Gly	Ser	Gly	Asn	Trp	Pro	Asp	Gly	Ser	Asn	Ile	
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Gly	Phe	Met	Pro	Lys												
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Leu	Thr	Thr	Ile	Gly	Leu	Leu	Leu	Gln	Ile	Thr	Ser	Leu	Cys	Ser	Ile	
			20					25					30			
Trp	Phe	Ser	His	Tyr	Asn	Gln	Val	Thr	Gln	Pro	His	Glu	Gln	Ala	Cys	
		35					40					45				
Ser	Asn	Asn	Thr	Thr	Asn	Tyr	Tyr	Asn	Glu	Thr	Phe	Val	Asn	Val	Thr	
	50					55					60					
Asn	Val	Gln	Asn	Asn	Tyr	Thr	Thr	Ile	Ile	Glu	Pro	Ser	Ala	Pro	Asn	
65					70					75					80	
Val	Val	His	Tyr	Ser	Ser	Gly	Arg	Asp	Leu	Cys	Pro	Val	Lys	Gly	Trp	
				85					90					95		
Ala	Pro	Leu	Ser	Lys	Asp	Asn	Gly	Ile	Arg	Ile	Gly	Ser	Arg	Gly	Glu	
			100					105					110			
Val	Phe	Val	Ile	Arg	Glu	Pro	Phe	Ile	Ser	Cys	Ser	Ile	Ser	Glu	Cys	
		115					120					125				
Arg	Thr	Phe	Phe	Leu	Thr	Gln	Gly	Ala	Leu	Leu	Asn	Asp	Lys	His	Ser	
	130					135					140					
Asn	Gly	Thr	Val	Lys	Asp	Arg	Ser	Pro	Phe	Arg	Thr	Leu	Met	Ser	Cys	
145					150					155					160	
Pro	Met	Gly	Val	Ala	Pro	Ser	Pro	Ser	Asn	Ser	Arg	Phe	Glu	Ser	Val	
				165					170					175		
Ala	Trp	Ser	Ala	Thr	Ala	Cys	Ser	Asp	Gly	Pro	Gly	Trp	Leu	Thr	Leu	
			180					185					190			
Gly	Ile	Thr	Gly	Pro	Asp	Ala	Thr	Ala	Val	Ala	Val	Leu	Lys	Tyr	Asn	
		195					200					205				
Gly	Ile	Ile	Thr	Asp	Thr	Leu	Lys	Ser	Trp	Lys	Gly	Asn	Ile	Met	Arg	
	210					215					220					
Thr	Gln	Glu	Ser	Glu	Cys	Val	Cys	Gln	Asp	Glu	Phe	Cys	Tyr	Thr	Leu	
225					230					235					240	
Ile	Thr	Asp	Gly	Pro	Ser	Asn	Ala	Gln	Ala	Phe	Tyr	Lys	Ile	Leu	Lys	
				245					250					255		
Ile	Arg	Lys	Gly	Lys	Ile	Val	Ser	Val	Lys	Asp	Val	Asn	Ala	Thr	Gly	
			260					265					270			
Phe	His	Phe	Glu	Glu	Cys	Ser	Cys	Tyr	Pro	Ser	Gly	Thr	Asp	Val	Glu	
		275					280					285				
Cys	Val	Cys	Arg	Asp	Asn	Trp	Arg	Gly	Ser	Asn	Arg	Pro	Trp	Ile	Arg	
	290					295					300					
Phe	Asn	Ser	Asp	Leu	Asp	Tyr	Gln	Ile	Gly	Tyr	Val	Cys	Ser	Gly	Ile	
305					310					315					320	
Phe	Gly	Asp	Asn	Pro	Arg	Pro	Val	Asp	Gly	Ile	Gly	Ser	Cys	Asn	Ser	
				325					330					335		
Pro	Val	Asn	Asn	Gly	Lys	Gly	Arg	Tyr	Gly	Val	Lys	Gly	Phe	Ser	Phe	
			340					345					350			
Arg	Tyr	Gly	Asp	Gly	Val	Trp	Ile	Gly	Arg	Thr	Lys	Ser	Leu	Glu	Ser	
		355					360					365				
Arg	Ser	Gly	Phe	Glu	Met	Val	Trp	Asp	Ala	Asn	Gly	Trp	Val	Ser	Thr	
	370						375				380					
Asp	Lys	Asp	Ser	Asn	Gly	Val	Gln	Asp	Ile	Ile	Asp	Asn	Asn	Asn	Trp	
385					390					395					400	
Ser	Gly	Tyr	Ser	Gly	Ser	Phe	Ser	Ile	Arg	Trp	Glu	Thr	Thr	Gly	Arg	
				405					410					415		
Asn	Cys	Thr	Val	Pro	Cys	Phe	Trp	Val	Glu	Met	Ile	Arg	Gly	Gln	Pro	

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420				425				430							
Lys	Glu	Lys	Thr	Ile	Trp	Thr	Ser	Gly	Ser	Ser	Ile	Ala	Phe	Cys	Gly
435				440				445							
Val	Asn	Ser	Asp	Thr	Thr	Gly	Trp	Ser	Trp	Pro	Asp	Gly	Ala	Leu	Leu
450				455				460							
Pro	Phe	Asp	Ile	Asp	Lys										
465				470											
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1	5				10				15						
Leu	Val	Ile	Phe	Asn	Ile	Leu	Leu	His	Val	Ala	Ser	Ile	Thr	Leu	Gly
20				25				30							
Ile	Ile	Ser	Val	Thr	Lys	Asp	Asn	Lys	Val	His	Ile	Cys	Asn	Thr	Thr
35				40				45							
Glu	Val	Tyr	Asn	Glu	Thr	Val	Arg	Val	Glu	Thr	Val	Val	Ile	Pro	Val
50				55				60							
Asn	Asn	Thr	Ile	Tyr	Leu	Asn	His	Glu	Pro	Glu	Phe	Leu	Asn	Asn	Thr
65				70				75				80			
Glu	Pro	Leu	Cys	Asp	Val	Ser	Gly	Phe	Ala	Ile	Val	Ser	Lys	Asp	Asn
85				90				95							
Gly	Ile	Arg	Ile	Gly	Ser	Arg	Gly	His	Ile	Phe	Val	Ile	Arg	Glu	Pro
100				105				110							
Phe	Val	Ser	Cys	Gly	Pro	Ser	Glu	Cys	Arg	Thr	Phe	Phe	Leu	Thr	Gln
115				120				125							
Gly	Ala	Leu	Leu	Asn	Asp	Lys	His	Ser	Asn	Asn	Thr	Val	Lys	Asp	Arg
130				135				140							
Ser	Pro	Tyr	Arg	Ala	Leu	Met	Ser	Val	Pro	Leu	Gly	Ser	Ser	Pro	Asn
145				150				155				160			
Ala	Tyr	Gln	Ala	Lys	Phe	Glu	Ser	Val	Gly	Trp	Ser	Ala	Thr	Ala	Cys
165				170				175							
His	Asp	Gly	Lys	Lys	Trp	Met	Ala	Ile	Gly	Val	Ser	Gly	Ala	Asp	Asp
180				185				190							
Asp	Ala	Tyr	Ala	Val	Ile	His	Tyr	Gly	Gly	Val	Pro	Thr	Asp	Val	Ile
195				200				205							
Arg	Ser	Trp	Arg	Lys	Gln	Ile	Leu	Arg	Thr	Gln	Glu	Ser	Ser	Cys	Val
210				215				220							
Cys	Ile	Lys	Gly	Glu	Cys	Tyr	Trp	Val	Met	Thr	Asp	Gly	Pro	Ala	Asn
225				230				235				240			
Asn	Gln	Ala	Ser	Tyr	Lys	Ile	Phe	Lys	Ser	Gln	Lys	Gly	Met	Val	Val
245				250				255							
Asp	Glu	Lys	Glu	Ile	Ser	Phe	Gln	Gly	Gly	His	Ile	Glu	Glu	Cys	Ser
260				265				270							
Cys	Tyr	Pro	Asn	Met	Gly	Lys	Val	Glu	Cys	Val	Cys	Arg	Asp	Asn	Trp
275				280				285							

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Asn	Gly	Met	Asn	Arg	Pro	Ile	Leu	Ile	Phe	Asp	Glu	Lys	Leu	Glu	Tyr	
290						295				300						
Glu	Val	Gly	Tyr	Leu	Cys	Ala	Gly	Ile	Pro	Thr	Asp	Thr	Pro	Arg	Val	
305					310				315					320		
Gln	Asp	Ser	Ser	Phe	Thr	Gly	Ser	Cys	Thr	Asn	Ala	Val	Gly	Arg	Ser	
				325				330						335		
Gly	Thr	Asn	Asn	Tyr	Gly	Val	Lys	Gly	Phe	Gly	Phe	Arg	Gln	Gly	Asn	
			340					345					350			
Ser	Val	Trp	Ala	Gly	Arg	Thr	Ile	Ser	Val	Ser	Ser	Arg	Ser	Gly	Phe	
		355					360					365				
Glu	Val	Leu	Leu	Ile	Glu	Asp	Gly	Trp	Ile	Arg	Pro	Ser	Lys	Thr	Ile	
	370					375					380					
Ser	Lys	Lys	Val	Glu	Val	Leu	Asn	Asn	Lys	Asn	Trp	Ser	Gly	Tyr	Ser	
385					390					395					400	
Gly	Ala	Phe	Thr	Ile	Pro	Thr	Ala	Met	Thr	Ser	Lys	Asn	Cys	Ile	Val	
				405					410					415		
Pro	Cys	Phe	Trp	Leu	Glu	Met	Ile	Arg	Gly	Lys	Pro	Glu	Glu	Arg	Thr	
			420					425					430			
Ser	Ile	Trp	Thr	Ser	Ser	Ser	Ser	Thr	Val	Phe	Cys	Gly	Val	Ser	Ser	
		435					440					445				
Glu	Val	Pro	Gly	Trp	Ser	Trp	Asp	Asp	Gly	Ala	Ile	Leu	Pro	Phe	Asp	
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Ile	Asp	Lys	Met													
465																
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Leu	Ser	Val	Val	Ser	Leu	Leu	Val	Gly	Ile	Ala	Asn	Leu	Gly	Leu	Asn	
			20					25					30			
Ile	Gly	Leu	His	Tyr	Lys	Val	Gly	Asp	Thr	Pro	Asn	Val	Asn	Ile	Pro	
		35					40					45				
Asn	Val	Asn	Gly	Thr	Asn	Ser	Thr	Thr	Thr	Ile	Ile	Asn	Asn	Asn	Thr	
	50					55				60						
Gln	Asn	Asn	Phe	Thr	Asn	Ile	Thr	Asn	Ile	Ile	Gln	Ser	Lys	Gly	Gly	
65					70				75						80	
Glu	Arg	Thr	Phe	Leu	Asn	Leu	Thr	Lys	Pro	Leu	Cys	Glu	Val	Asn	Ser	
				85				90						95		
Trp	His	Ile	Leu	Ser	Lys	Asp	Asn	Ala	Ile	Arg	Ile	Gly	Glu	Asp	Ala	
			100				105						110			
His	Ile	Leu	Val	Thr	Arg	Glu	Pro	Tyr	Leu	Ser	Cys	Asp	Pro	Gln	Gly	
		115					120					125				
Cys	Arg	Met	Phe	Ala	Leu	Ser	Gln	Gly	Thr	Thr	Leu	Arg	Gly	Arg	His	
	130						135					140				

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145					150					155					160	
Trp	Glu	Met	Gly	Gln	Ala	Pro	Ser	Pro	Tyr	Asn	Thr	Arg	Val	Glu	Cys	
				165					170					175		
Ile	Gly	Trp	Ser	Ser	Thr	Ser	Cys	His	Asp	Gly	Met	Ser	Arg	Met	Ser	
			180					185					190			
Ile	Cys	Met	Ser	Gly	Pro	Asn	Asn	Asn	Ala	Ser	Ala	Val	Val	Trp	Tyr	
		195					200					205				
Gly	Gly	Arg	Pro	Ile	Thr	Glu	Ile	Pro	Ser	Trp	Ala	Gly	Asn	Ile	Leu	
	210					215					220					
Arg	Thr	Gln	Glu	Ser	Glu	Cys	Val	Cys	His	Lys	Gly	Val	Cys	Pro	Val	
225					230					235					240	
Val	Met	Thr	Asp	Gly	Pro	Ala	Asn	Asn	Arg	Ala	Ala	Thr	Lys	Ile	Ile	
				245					250					255		
Tyr	Phe	Lys	Glu	Gly	Lys	Ile	Gln	Lys	Ile	Glu	Glu	Leu	Ala	Gly	Asn	
			260					265					270			
Ala	Gln	His	Ile	Glu	Glu	Cys	Ser	Cys	Tyr	Gly	Ala	Gly	Gly	Val	Ile	
		275					280					285				
Lys	Cys	Ile	Cys	Arg	Asp	Asn	Trp	Lys	Gly	Ala	Asn	Arg	Pro	Val	Ile	
	290					295					300					
Thr	Ile	Asp	Pro	Glu	Met	Met	Thr	His	Thr	Ser	Lys	Tyr	Leu	Cys	Ser	
305					310					315					320	
Lys	Val	Leu	Thr	Asp	Thr	Ser	Arg	Pro	Asn	Asp	Pro	Thr	Asn	Gly	Asn	
				325					330					335		
Cys	Asp	Ala	Pro	Ile	Thr	Gly	Gly	Ser	Pro	Asp	Pro	Gly	Val	Lys	Gly	
			340					345					350			
Phe	Ala	Phe	Leu	Asp	Gly	Glu	Asn	Ser	Trp	Leu	Gly	Arg	Thr	Ile	Ser	
		355					360					365				
Lys	Asp	Ser	Arg	Ser	Gly	Tyr	Glu	Met	Leu	Lys	Val	Pro	Asn	Ala	Glu	
	370					375					380					
Thr	Asp	Ile	Gln	Ser	Gly	Pro	Ile	Ser	Asn	Gln	Val	Ile	Val	Asn	Asn	
385					390					395					400	
Gln	Asn	Trp	Ser	Gly	Tyr	Ser	Gly	Ala	Phe	Ile	Asp	Tyr	Trp	Ala	Asn	
			405						410					415		
Lys	Glu	Cys	Phe	Asn	Pro	Cys	Phe	Tyr	Val	Glu	Leu	Ile	Arg	Gly	Arg	
			420					425					430			
Pro	Lys	Glu	Ser	Ser	Val	Leu	Trp	Thr	Ser	Asn	Ser	Ile	Val	Ala	Leu	
		435					440					445				
Cys	Gly	Ser	Lys	Lys	Arg	Leu	Gly	Ser	Trp	Ser	Trp	His	Asp	Gly	Ala	
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Glu	Ile	Ile	Tyr	Phe	Glu											
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1	5					10					15				
Leu	Ser	Val	Leu	Asn	Leu	Leu	Ile	Gly	Ile	Ser	Asn	Val	Gly	Leu	Asn
			20					25					30		
Val	Ser	Leu	His	Leu	Lys	Gly	Glu	Gly	Val	Lys	Gln	Glu	Asn	Asn	Leu
		35					40					45			
Thr	Cys	Thr	Thr	Ile	Thr	Gln	Asn	Asn	Thr	Thr	Val	Val	Glu	Asn	Thr
	50					55					60				
Tyr	Val	Asn	Asn	Thr	Thr	Ile	Ile	Asn	Lys	Gly	Thr	Asn	Leu	Lys	Ala
65					70					75					80
Pro	Asn	Tyr	Leu	Leu	Leu	Asn	Lys	Ser	Leu	Cys	Ser	Val	Glu	Gly	Trp
			85					90						95	
Val	Val	Ile	Ala	Lys	Asp	Asn	Ala	Ile	Arg	Phe	Gly	Glu	Ser	Glu	Gln
			100					105					110		
Ile	Ile	Val	Thr	Arg	Glu	Pro	Tyr	Val	Ser	Cys	Asp	Pro	Ser	Gly	Cys
		115					120					125			
Lys	Met	Tyr	Ala	Leu	His	Gln	Gly	Thr	Thr	Ile	Arg	Asn	Lys	His	Ser
	130					135					140				
Asn	Gly	Thr	Ile	His	Asp	Arg	Thr	Thr	Phe	Arg	Gly	Leu	Ile	Ser	Thr
145					150					155					160
Pro	Leu	Gly	Thr	Pro	Pro	Thr	Val	Ser	Asn	Ser	Asp	Phe	Ile	Cys	Val
				165					170					175	
Gly	Trp	Ser	Ser	Thr	Ser	Cys	His	Asp	Gly	Val	Gly	Arg	Met	Thr	Ile
			180					185					190		
Cys	Ile	Gln	Gly	Asn	Asn	Asp	Asn	Ala	Thr	Ala	Thr	Val	Tyr	Tyr	Asn
		195					200					205			
Arg	Arg	Leu	Thr	Thr	Thr	Ile	Lys	Thr	Trp	Ala	Lys	Asn	Ile	Leu	Arg
		210				215						220			
Thr	Gln	Glu	Ser	Glu	Cys	Val	Cys	Tyr	Asn	Gly	Thr	Cys	Ala	Val	Val
225					230					235					240
Met	Thr	Asp	Gly	Pro	Ala	Ser	Ser	Gln	Ala	Tyr	Thr	Lys	Ile	Met	Tyr
				245					250					255	
Phe	His	Lys	Gly	Leu	Ile	Ile	Lys	Glu	Glu	Pro	Leu	Arg	Gly	Ser	Ala
			260					265					270		
Arg	His	Ile	Glu	Glu	Cys	Ser	Cys	Tyr	Gly	His	Asp	Gln	Lys	Val	Ser
		275					280					285			
Cys	Val	Cys	Arg	Asp	Asn	Trp	Gln	Gly	Ala	Asn	Arg	Pro	Ile	Ile	Glu
		290				295						300			
Ile	Asp	Met	Ser	Thr	Leu	Glu	His	Thr	Ser	Arg	Cys	Val	Cys	Thr	Gly
305					310					315					320
Val	Leu	Thr	Asp	Thr	Ser	Arg	Pro	Gly	Asp	Lys	Pro	Asn	Gly	Asp	Cys
				325					330					335	
Ser	Asn	Pro	Ile	Thr	Gly	Ser	Pro	Gly	Ala	Pro	Gly	Val	Lys	Gly	Phe
			340					345					350		
Gly	Phe	Leu	Asn	Gly	Asp	Asn	Thr	Trp	Leu	Gly	Arg	Thr	Ile	Ser	Pro
		355					360					365			
Arg	Ser	Arg	Ser	Gly	Phe	Glu	Met	Leu	Lys	Ile	Pro	Asn	Ala	Glu	Thr
					375						380				
Asp	Pro	Asn	Ser	Arg	Ile	Ile	Glu	Arg	Gln	Glu	Ile	Val	Asp	Asn	Ser
385					390					395					400
Asn	Trp	Ser	Gly	Tyr	Ser	Gly	Ser	Phe	Ile	Asp	Cys	Trp	Asp	Glu	Ala
				405					410					415	

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Asn	Glu	Cys	Tyr	Asn	Pro	Cys	Phe	Tyr	Val	Glu	Leu	Ile	Arg	Gly	Arg	
			420					425					430			
Pro	Glu	Glu	Ala	Lys	Tyr	Val	Trp	Trp	Thr	Ser	Asn	Ser	Leu	Ile	Ala	
			435				440					445				
Leu	Cys	Gly	Ser	Pro	Val	Ser	Val	Gly	Ser	Gly	Ser	Phe	Pro	Asp	Gly	
	450					455					460					
Ala	Gln	Ile	Gln	Tyr	Phe	Ser										
465					470											
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<211> LENGTH: 470																
<212> TYPE: PRT																
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<221> NAME/KEY: MISC_FEATURE																
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<223> OTHER INFORMATION: NA Type 8																
<400> SEQUENCE: 24																
Met	Asn	Pro	Asn	Gln	Lys	Ile	Ile	Thr	Ile	Gly	Ser	Ile	Ser	Leu	Gly	
1				5				10						15		
Leu	Val	Val	Phe	Asn	Val	Leu	Leu	His	Val	Val	Ser	Ile	Ile	Val	Thr	
			20					25					30			
Val	Leu	Val	Leu	Gly	Lys	Gly	Gly	Asn	Asn	Gly	Ile	Cys	Asn	Glu	Thr	
			35				40					45				
Val	Val	Arg	Glu	Tyr	Asn	Glu	Thr	Val	Arg	Ile	Glu	Lys	Val	Thr	Gln	
	50					55				60						
Trp	His	Asn	Thr	Asn	Val	Val	Glu	Tyr	Val	Pro	Tyr	Trp	Asn	Gly	Gly	
65				70					75					80		
Thr	Tyr	Met	Asn	Asn	Thr	Glu	Ala	Ile	Cys	Asp	Ala	Lys	Gly	Phe	Ala	
			85					90						95		
Pro	Phe	Ser	Lys	Asp	Asn	Gly	Ile	Arg	Ile	Gly	Ser	Arg	Gly	His	Ile	
			100					105					110			
Phe	Val	Ile	Arg	Glu	Pro	Phe	Val	Ser	Cys	Ser	Pro	Ile	Glu	Cys	Arg	
			115				120					125				
Thr	Phe	Phe	Leu	Thr	Gln	Gly	Ser	Leu	Leu	Asn	Asp	Lys	His	Ser	Asn	
					135					140						
Gly	Thr	Val	Lys	Asp	Arg	Ser	Pro	Phe	Arg	Thr	Leu	Met	Ser	Val	Glu	
145				150						155					160	
Val	Gly	Gln	Ser	Pro	Asn	Val	Tyr	Gln	Ala	Arg	Phe	Glu	Ala	Val	Ala	
				165					170					175		
Trp	Ser	Ala	Thr	Ala	Cys	His	Asp	Gly	Lys	Lys	Trp	Met	Thr	Val	Gly	
			180					185					190			
Val	Thr	Gly	Pro	Asp	Ser	Lys	Ala	Val	Ala	Val	Ile	His	Tyr	Gly	Gly	
			195				200					205				
Val	Pro	Thr	Asp	Val	Val	Asn	Ser	Trp	Ala	Gly	Asp	Ile	Leu	Arg	Thr	
			210				215				220					
Gln	Glu	Ser	Ser	Cys	Thr	Cys	Ile	Gln	Gly	Asp	Cys	Tyr	Trp	Val	Met	
225				230						235					240	
Thr	Asp	Gly	Pro	Ala	Asn	Arg	Gln	Ala	Gln	Tyr	Arg	Ile	Tyr	Lys	Ala	
				245					250					255		
Asn	Gln	Gly	Arg	Ile	Ile	Gly	Gln	Thr	Asp	Ile	Ser	Phe	Asn	Gly	Gly	
			260					265					270			

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His	Ile	Glu	Glu	Cys	Ser	Cys	Tyr	Pro	Asn	Asp	Gly	Lys	Val	Glu	Cys	
		275					280					285				
Val	Cys	Arg	Asp	Gly	Trp	Thr	Gly	Thr	Asn	Arg	Pro	Val	Leu	Val	Ile	
	290					295					300					
Ser	Pro	Asp	Leu	Ser	Tyr	Arg	Val	Gly	Tyr	Leu	Cys	Ala	Gly	Ile	Pro	
305					310					315					320	
Ser	Asp	Thr	Pro	Arg	Gly	Glu	Asp	Thr	Gln	Phe	Thr	Gly	Ser	Cys	Thr	
				325					330					335		
Ser	Pro	Met	Gly	Asn	Gln	Gly	Tyr	Gly	Val	Lys	Gly	Phe	Gly	Phe	Arg	
			340					345					350			
Gln	Gly	Thr	Asp	Val	Trp	Met	Gly	Arg	Thr	Ile	Ser	Arg	Thr	Ser	Arg	
		355					360					365				
Ser	Gly	Phe	Glu	Ile	Leu	Arg	Ile	Lys	Asn	Gly	Trp	Thr	Gln	Thr	Ser	
	370					375					380					
Lys	Glu	Gln	Ile	Arg	Lys	Gln	Val	Val	Val	Asp	Asn	Leu	Asn	Trp	Ser	
385						390				395					400	
Gly	Tyr	Ser	Gly	Ser	Phe	Thr	Leu	Pro	Val	Glu	Leu	Ser	Gly	Lys	Asp	
				405					410					415		
Cys	Leu	Val	Pro	Cys	Phe	Trp	Val	Glu	Met	Ile	Arg	Gly	Lys	Pro	Glu	
			420					425					430			
Glu	Lys	Thr	Ile	Trp	Thr	Ser	Ser	Ser	Ser	Ile	Val	Met	Cys	Gly	Val	
		435					440					445				
Asp	Tyr	Glu	Val	Ala	Asp	Trp	Ser	Trp	His	Asp	Gly	Ala	Ile	Leu	Pro	
	450					455					460					
Phe	Asp	Ile	Asp	Lys	Met											
465					470											
<210> SEQ ID NO 25																
<211> LENGTH: 470																
<212> TYPE: PRT																
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<220> FEATURE:																
<221> NAME/KEY: MISC_FEATURE																
<222> LOCATION: (1)..(470)																
<223> OTHER INFORMATION: NA Type 9																
<400> SEQUENCE: 25																
Met	Asn	Pro	Asn	Gln	Lys	Ile	Leu	Cys	Thr	Ser	Ala	Thr	Ala	Leu	Val	
1				5					10					15		
Ile	Gly	Thr	Ile	Ala	Val	Leu	Ile	Gly	Ile	Thr	Asn	Leu	Gly	Leu	Asn	
		20						25					30			
Ile	Gly	Leu	His	Leu	Lys	Pro	Ser	Cys	Asn	Cys	Ser	His	Ser	Gln	Pro	
		35					40					45				
Glu	Ala	Thr	Asn	Ala	Ser	Gln	Thr	Ile	Ile	Asn	Asn	Tyr	Tyr	Asn	Asp	
	50					55					60					
Thr	Asn	Ile	Thr	Gln	Ile	Ser	Asn	Thr	Asn	Ile	Gln	Val	Glu	Glu	Arg	
65					70					75					80	
Ala	Ile	Arg	Asp	Phe	Asn	Asn	Leu	Thr	Lys	Gly	Leu	Cys	Thr	Ile	Asn	
				85					90					95		
Ser	Trp	His	Ile	Tyr	Gly	Lys	Asp	Asn	Ala	Val	Arg	Ile	Gly	Glu	Asp	
		100						105					110			
Ser	Asp	Val	Leu	Val	Thr	Arg	Glu	Pro	Tyr	Val	Ser	Cys	Asp	Pro	Asp	
		115					120					125				
Glu	Cys	Arg	Phe	Tyr	Ala	Leu	Ser	Gln	Gly	Thr	Thr	Ile	Arg	Gly	Lys	

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<210> SEQ ID NO 26
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Influenza A virus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(252)
<223> OTHER INFORMATION: M1

<400> SEQUENCE: 26
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Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr	Tyr	Val	Leu	Ser	Ile	Ile	Pro
1				5					10					15	
Ser	Gly	Pro	Leu	Lys	Ala	Glu	Ile	Ala	Gln	Lys	Leu	Glu	Asp	Val	Phe
			20					25					30		
Ala	Gly	Lys	Asn	Thr	Asp	Leu	Glu	Ala	Leu	Met	Glu	Trp	Leu	Lys	Thr
		35					40					45			
Arg	Pro	Ile	Leu	Ser	Pro	Leu	Thr	Lys	Gly	Ile	Leu	Gly	Phe	Val	Phe
	50					55					60				
Thr	Leu	Thr	Val	Pro	Ser	Glu	Arg	Gly	Leu	Gln	Arg	Arg	Arg	Phe	Val
65					70					75					80
Gln	Asn	Ala	Leu	Asn	Gly	Asn	Gly	Asp	Pro	Asn	Asn	Met	Asp	Arg	Ala
				85					90					95	
Val	Lys	Leu	Tyr	Lys	Lys	Leu	Lys	Arg	Glu	Ile	Thr	Phe	His	Gly	Ala
			100					105					110		
Lys	Glu	Val	Ala	Leu	Ser	Tyr	Ser	Thr	Gly	Ala	Leu	Ala	Ser	Cys	Met
		115					120					125			
Gly	Leu	Ile	Tyr	Asn	Arg	Met	Gly	Thr	Val	Thr	Thr	Glu	Val	Ala	Phe
	130					135					140				
Gly	Leu	Val	Cys	Ala	Thr	Cys	Glu	Gln	Ile	Ala	Asp	Ser	Gln	His	Arg
145					150					155					160
Ser	His	Arg	Gln	Met	Ala	Thr	Thr	Thr	Asn	Pro	Leu	Ile	Arg	His	Glu
				165					170					175	
Asn	Arg	Met	Val	Leu	Ala	Ser	Thr	Thr	Ala	Lys	Ala	Met	Glu	Gln	Met
			180					185					190		
Ala	Gly	Ser	Ser	Glu	Gln	Ala	Ala	Glu	Ala	Met	Glu	Ile	Ala	Asn	Gln
		195					200					205			
Ala	Arg	Gln	Met	Val	Gln	Ala	Met	Arg	Thr	Ile	Gly	Thr	His	Pro	Asn
	210					215					220				
Ser	Ser	Ala	Gly	Leu	Arg	Asp	Asn	Leu	Leu	Glu	Asn	Leu	Gln	Ala	Tyr
225					230					235					240
Gln	Lys	Arg	Met	Gly	Val	Gln	Met	Gln	Arg	Phe	Lys				
				245					250						
<210> SEQ ID NO 27															
<211> LENGTH: 97															
<212> TYPE: PRT															
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<221> NAME/KEY: MISC_FEATURE															
<222> LOCATION: (1)..(97)															
<223> OTHER INFORMATION: M2															
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Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr	Pro	Thr	Arg	Thr	Glu	Trp	Glu
1				5					10					15	
Cys	Arg	Cys	Ser	Asp	Ser	Ser	Asp	Pro	Leu	Val	Val	Ala	Ala	Asn	Ile
			20					25					30		
Ile	Gly	Ile	Leu	His	Leu	Ile	Leu	Trp	Ile	Leu	Asp	Arg	Leu	Phe	Phe
		35					40					45			
Lys	Cys	Ile	Tyr	Arg	Arg	Leu	Lys	Tyr	Gly	Leu	Lys	Ile	Gly	Pro	Ser
	50					55					60				
Thr	Glu	Gly	Val	Pro	Glu	Ser	Met	Arg	Glu	Glu	Tyr	Arg	Gln	Glu	Gln
65					70					75					80

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Gln	Ser	Ala	Val	Asp	Val	Asp	Asp	Gly	His	Phe	Val	Asn	Ile	Glu	Leu
			85						90					95	
Glu															
<210> SEQ ID NO 28															
<211> LENGTH: 566															
<212> TYPE: PRT															
<213> ORGANISM: Influenza A virus															
<220> FEATURE:															
<221> NAME/KEY: MISC_FEATURE															
<222> LOCATION: (1)..(566)															
<223> OTHER INFORMATION: HA from H1N1 (A/Hawaii/70/2019)															
<400> SEQUENCE: 28															
Met	Lys	Ala	Ile	Leu	Val	Val	Leu	Leu	Tyr	Thr	Phe	Thr	Thr	Ala	Asn
1				5					10					15	
Ala	Asp	Thr	Leu	Cys	Ile	Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Asp	Thr
			20					25					30		
Val	Asp	Thr	Val	Leu	Glu	Lys	Asn	Val	Thr	Val	Thr	His	Ser	Val	Asn
			35				40					45			
Leu	Leu	Glu	Asp	Lys	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu	Arg	Gly	Val
			50			55					60				
Ala	Pro	Leu	His	Leu	Gly	Lys	Cys	Asn	Ile	Ala	Gly	Trp	Ile	Leu	Gly
65				70						75				80	
Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Arg	Ser	Trp	Ser	Tyr	Ile
				85					90					95	
Val	Glu	Thr	Ser	Asn	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro	Gly	Asp	Phe
			100					105					110		
Ile	Asn	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val	Ser	Ser	Phe
			115				120					125			
Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro	Asn	His	Asp
			130				135				140				
Ser	Asp	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly	Ala	Lys	Ser
145				150						155				160	
Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Lys	Lys	Gly	Asn	Ser	Tyr	Pro
			165					170					175		
Lys	Leu	Asn	Gln	Thr	Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu	Val	Leu	Val
			180					185					190		
Leu	Trp	Gly	Ile	His	His	Pro	Pro	Thr	Ile	Ala	Ala	Gln	Glu	Ser	Leu
			195				200					205			
Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Thr	Ser	Arg	Tyr	Ser
			210				215				220				
Lys	Lys	Phe	Lys	Pro	Glu	Ile	Ala	Thr	Arg	Pro	Lys	Val	Arg	Asp	Gln
225				230						235				240	
Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro	Gly	Asp	Lys
				245					250					255	
Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe
			260					265					270		
Thr	Met	Glu	Arg	Asp	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser	Asp	Thr	Pro
			275				280					285			
Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Glu	Gly	Ala	Ile	Asn
			290				295				300				
Thr	Ser	Leu	Pro	Phe	Gln	Asn	Val	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys
305				310						315				320	

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Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg	
				325					330					335		
Asn	Val	Pro	Ser	Ile	Gln	Ser	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	
			340					345					350			
Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	
		355					360					365				
His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser	
	370					375					380					
Thr	Gln	Asn	Ala	Ile	Asp	Lys	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	
385					390					395					400	
Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His	
				405					410					415		
Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	
			420					425					430			
Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	
	435					440						445				
Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	
	450					455					460					
Lys	Val	Arg	Asn	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	
465				470						475					480	
Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	
				485				490						495		
Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	
			500					505					510			
Asn	Arg	Glu	Lys	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	
		515					520					525				
Gln	Ile	Leu	Ala	Ile	Tyr	Ser	Thr	Val	Ala	Ser	Ser	Leu	Val	Leu	Val	
	530					535					540					
Val	Ser	Leu	Gly	Ala	Ile	Ser	Phe	Trp	Met	Cys	Ser	Asn	Gly	Ser	Leu	
545					550					555					560	
Gln	Cys	Arg	Ile	Cys	Ile											
				565												
<210> SEQ ID NO 29																
<211> LENGTH: 566																
<212> TYPE: PRT																
<213> ORGANISM: Influenza A virus																
<220> FEATURE:																
<221> NAME/KEY: MISC_FEATURE																
<222> LOCATION: (1)..(566)																
<223> OTHER INFORMATION: HA from H3N2 (A/Kansas/14/2017)																
<400> SEQUENCE: 29																
Met	Lys	Thr	Ile	Ile	Ala	Leu	Ser	Cys	Ile	Leu	Cys	Leu	Val	Phe	Ala	
1				5					10					15		
Gln	Lys	Ile	Pro	Gly	Asn	Asp	Asn	Ser	Thr	Ala	Thr	Leu	Cys	Leu	Gly	
			20				25						30			
His	His	Ala	Val	Pro	Asn	Gly	Thr	Ile	Val	Lys	Thr	Ile	Thr	Asn	Asp	
	35						40					45				
Arg	Ile	Glu	Val	Thr	Asn	Ala	Thr	Glu	Leu	Val	Gln	Asn	Ser	Ser	Ile	
	50				55						60					
Gly	Glu	Ile	Cys	Asp	Ser	Pro	His	Gln	Ile	Leu	Asp	Gly	Glu	Asn	Cys	
65					70				75					80		

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Thr	Leu	Ile	Asp	Ala	Leu	Leu	Gly	Asp	Pro	Gln	Cys	Asp	Gly	Phe	Gln	
			85					90					95			
Asn	Lys	Lys	Trp	Asp	Leu	Phe	Val	Glu	Arg	Asn	Lys	Ala	Tyr	Ser	Asn	
			100					105					110			
Cys	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser	Leu	Arg	Ser	Leu	Val	
		115					120					125				
Ala	Ser	Ser	Gly	Thr	Leu	Glu	Phe	Asn	Asn	Glu	Ser	Phe	Asn	Trp	Ala	
	130					135					140					
Gly	Val	Thr	Gln	Asn	Gly	Thr	Ser	Ser	Ser	Cys	Ile	Arg	Gly	Ser	Lys	
145					150					155					160	
Ser	Ser	Phe	Phe	Ser	Arg	Leu	Asn	Trp	Leu	Thr	His	Leu	Asn	Ser	Lys	
			165					170						175		
Tyr	Pro	Ala	Leu	Asn	Val	Thr	Met	Pro	Asn	Asn	Glu	Gln	Phe	Asp	Lys	
			180					185					190			
Leu	Tyr	Ile	Trp	Gly	Val	His	His	Pro	Gly	Thr	Asp	Lys	Asp	Gln	Ile	
		195					200					205				
Ser	Leu	Tyr	Ala	Gln	Ser	Ser	Gly	Arg	Ile	Thr	Val	Ser	Thr	Lys	Arg	
	210					215					220					
Ser	Gln	Gln	Ala	Val	Ile	Pro	Asn	Ile	Gly	Ser	Arg	Pro	Arg	Ile	Arg	
225					230					235					240	
Asp	Ile	Pro	Ser	Arg	Ile	Ser	Ile	Tyr	Trp	Thr	Ile	Val	Lys	Pro	Gly	
				245					250					255		
Asp	Ile	Leu	Leu	Ile	Asn	Ser	Thr	Gly	Asn	Leu	Ile	Ala	Pro	Arg	Gly	
			260					265					270			
Tyr	Phe	Lys	Ile	Arg	Ser	Gly	Lys	Ser	Ser	Ile	Met	Arg	Ser	Asp	Ala	
		275					280					285				
Pro	Ile	Gly	Lys	Cys	Lys	Ser	Glu	Cys	Ile	Thr	Pro	Asn	Gly	Ser	Ile	
	290					295					300					
Pro	Asn	Asp	Lys	Pro	Phe	Gln	Asn	Val	Asn	Arg	Ile	Thr	Tyr	Gly	Ala	
305					310					315					320	
Cys	Pro	Arg	Tyr	Val	Lys	Gln	Ser	Thr	Leu	Lys	Leu	Ala	Thr	Gly	Met	
				325					330					335		
Arg	Asn	Val	Pro	Glu	Arg	Gln	Thr	Arg	Gly	Ile	Phe	Gly	Ala	Ile	Ala	
			340					345					350			
Gly	Phe	Ile	Glu	Asn	Gly	Trp	Glu	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	
		355					360					365				
Phe	Arg	His	Gln	Asn	Ser	Glu	Gly	Arg	Gly	Gln	Ala	Ala	Asp	Leu	Lys	
	370						375				380					
Ser	Thr	Gln	Ala	Ala	Ile	Asp	Gln	Ile	Asn	Gly	Lys	Leu	Asn	Arg	Leu	
385					390					395					400	
Ile	Gly	Lys	Thr	Asn	Glu	Lys	Phe	His	Gln	Ile	Glu	Lys	Glu	Phe	Ser	
				405					410					415		
Glu	Val	Glu	Gly	Arg	Ile	Gln	Asp	Leu	Glu	Lys	Tyr	Val	Glu	Asp	Thr	
			420					425					430			
Lys	Ile	Asp	Leu	Trp	Ser	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Ala	Leu	Glu	
		435					440					445				
Asn	Gln	His	Thr	Ile	Asp	Leu	Thr	Asp	Ser	Glu	Met	Asn	Lys	Leu	Phe	
						455					460					
Glu	Lys	Thr	Lys	Lys	Gln	Leu	Arg	Glu	Asn	Ala	Glu	Asp	Met	Gly	Asn	
465					470					475					480	
Gly	Cys	Phe	Lys	Ile	Tyr	His	Lys	Cys	Asp	Asn	Ala	Cys	Met	Gly	Ser	

				485					490					495			
Ile	Arg	Asn	Gly	Thr	Tyr	Asp	His	Asn	Val	Tyr	Arg	Asp	Glu	Ala	Leu		
			500					505					510				
Asn	Asn	Arg	Phe	Gln	Ile	Lys	Gly	Val	Glu	Leu	Lys	Ser	Gly	Tyr	Lys		
		515					520					525					
Asp	Trp	Ile	Leu	Trp	Ile	Ser	Phe	Ala	Ile	Ser	Cys	Phe	Leu	Leu	Cys		
	530					535					540						
Val	Ala	Leu	Leu	Gly	Phe	Ile	Met	Trp	Ala	Cys	Gln	Lys	Gly	Asn	Ile		
545					550					555					560		
Arg	Cys	Asn	Ile	Cys	Ile												
				565													
<210> SEQ ID NO 30																	
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<223> OTHER INFORMATION: HA from H5N1 (A/Egypt/2321-NAMRU3/2007(H5N1))																	
<400> SEQUENCE: 30																	
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1				5					10					15			
Asp	Gln	Ile	Cys	Ile	Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Glu	Gln	Val		
			20					25					30				
Asp	Thr	Ile	Met	Glu	Lys	Asn	Val	Thr	Val	Thr	His	Ala	Gln	Asp	Ile		
		35					40					45					
Leu	Glu	Lys	Thr	His	Asn	Gly	Lys	Leu	Cys	Asp	Leu	Asp	Gly	Val	Lys		
	50					55					60						
Pro	Leu	Ile	Leu	Arg	Asp	Cys	Ser	Val	Ala	Gly	Trp	Leu	Leu	Gly	Asn		
65					70					75					80		
Pro	Met	Cys	Asp	Glu	Phe	Leu	Asn	Val	Pro	Glu	Trp	Ser	Tyr	Ile	Val		
				85					90					95			
Glu	Lys	Ile	Asn	Pro	Ala	Asn	Asp	Leu	Cys	Tyr	Pro	Gly	Asp	Phe	Asn		
			100					105					110				
Asp	Tyr	Glu	Glu	Leu	Lys	His	Leu	Leu	Ser	Arg	Ile	Asn	His	Phe	Glu		
		115					120					125					
Lys	Ile	Gln	Ile	Ile	Pro	Lys	Ser	Ser	Trp	Ser	Asp	Tyr	Glu	Ala	Ser		
	130					135					140						
Ser	Gly	Val	Ser	Ser	Ala	Cys	Pro	Tyr	Gln	Gly	Arg	Ser	Ser	Phe	Phe		
145					150					155					160		
Arg	Asn	Val	Val	Trp	Leu	Ile	Lys	Lys	Asn	Asn	Ala	Tyr	Pro	Thr	Ile		
				165					170						175		
Lys	Arg	Ser	Tyr	Asn	Asn	Thr	Asn	Gln	Glu	Asp	Leu	Leu	Val	Leu	Trp		
			180					185					190				
Gly	Ile	His	His	Pro	Asn	Asp	Ala	Ala	Glu	Gln	Ile	Arg	Leu	Tyr	Gln		
		195					200					205					
Asn	Pro	Thr	Thr	Tyr	Ile	Ser	Val	Gly	Thr	Ser	Thr	Leu	Asn	Gln	Arg		
	210					215											

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<210> SEQ ID NO 31
<211> LENGTH: 1255
<212> TYPE: PRT
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<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1255)
<223> OTHER INFORMATION: S protein

<400> SEQUENCE: 31
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Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15

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Asp	Arg	Cys	Thr	Thr	Phe	Asp	Asp	Val	Gln	Ala	Pro	Asn	Tyr	Thr	Gln	
			20					25					30			
His	Thr	Ser	Ser	Met	Arg	Gly	Val	Tyr	Tyr	Pro	Asp	Glu	Ile	Phe	Arg	
		35					40					45				
Ser	Asp	Thr	Leu	Tyr	Leu	Thr	Gln	Asp	Leu	Phe	Leu	Pro	Phe	Tyr	Ser	
	50					55					60					
Asn	Val	Thr	Gly	Phe	His	Thr	Ile	Asn	His	Thr	Phe	Gly	Asn	Pro	Val	
65					70					75					80	
Ile	Pro	Phe	Lys	Asp	Gly	Ile	Tyr	Phe	Ala	Ala	Thr	Glu	Lys	Ser	Asn	
				85					90					95		
Val	Val	Arg	Gly	Trp	Val	Phe	Gly	Ser	Thr	Met	Asn	Asn	Lys	Ser	Gln	
			100					105					110			
Ser	Val	Ile	Ile	Ile	Asn	Asn	Ser	Thr	Asn	Val	Val	Ile	Arg	Ala	Cys	
		115					120					125				
Asn	Phe	Glu	Leu	Cys	Asp	Asn	Pro	Phe	Phe	Ala	Val	Ser	Lys	Pro	Met	
	130					135					140					
Gly	Thr	Gln	Thr	His	Thr	Met	Ile	Phe	Asp	Asn	Ala	Phe	Asn	Cys	Thr	
145					150					155					160	
Phe	Glu	Tyr	Ile	Ser	Asp	Ala	Phe	Ser	Leu	Asp	Val	Ser	Glu	Lys	Ser	
				165					170					175		
Gly	Asn	Phe	Lys	His	Leu	Arg	Glu	Phe	Val	Phe	Lys	Asn	Lys	Asp	Gly	
			180					185					190			
Phe	Leu	Tyr	Val	Tyr	Lys	Gly	Tyr	Gln	Pro	Ile	Asp	Val	Val	Arg	Asp	
	195						200					205				
Leu	Pro	Ser	Gly	Phe	Asn	Thr	Leu	Lys	Pro	Ile	Phe	Lys	Leu	Pro	Leu	
	210					215					220					
Gly	Ile	Asn	Ile	Thr	Asn	Phe	Arg	Ala	Ile	Leu	Thr	Ala	Phe	Ser	Pro	
225					230					235					240	
Ala	Gln	Asp	Ile	Trp	Gly	Thr	Ser	Ala	Ala	Ala	Tyr	Phe	Val	Gly	Tyr	
			245						250					255		
Leu	Lys	Pro	Thr	Thr	Phe	Met	Leu	Lys	Tyr	Asp	Glu	Asn	Gly	Thr	Ile	
			260					265					270			
Thr	Asp	Ala	Val	Asp	Cys	Ser	Gln	Asn	Pro	Leu	Ala	Glu	Leu	Lys	Cys	
	275						280					285				
Ser	Val	Lys	Ser	Phe	Glu	Ile	Asp	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	
	290					295					300					
Phe	Arg	Val	Val	Pro	Ser	Gly	Asp	Val	Val	Arg	Phe	Pro	Asn	Ile	Thr	
305					310					315					320	
Asn	Leu	Cys	Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Lys	Phe	Pro	Ser	
			325						330					335		
Val	Tyr	Ala	Trp	Glu	Arg	Lys	Lys	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	
		340						345					350			
Ser	Val	Leu	Tyr	Asn	Ser	Thr	Phe	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	
	355					360						365				
Val	Ser	Ala	Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Ser	Asn	Val	Tyr	Ala	
	370					375					380					
Asp	Ser	Phe	Val	Val	Lys	Gly	Asp	Asp	Val	Arg	Gln	Ile	Ala	Pro	Gly	
385					390					395					400	
Gln	Thr	Gly	Val	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	
			405						410					415		
Met	Gly	Cys	Val	Leu	Ala	Trp	Asn	Thr	Arg	Asn	Ile	Asp	Ala	Thr	Ser	

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			420							425							430			
Thr	Gly	Asn	Tyr	Asn	Tyr	Lys	Tyr	Arg	Tyr	Leu	Arg	His	Gly	Lys	Leu					
		435					440					445								
Arg	Pro	Phe	Glu	Arg	Asp	Ile	Ser	Asn	Val	Pro	Phe	Ser	Pro	Asp	Gly					
		450				455					460									
Lys	Pro	Cys	Thr	Pro	Pro	Ala	Leu	Asn	Cys	Tyr	Trp	Pro	Leu	Asn	Asp					
		465				470				475					480					
Tyr	Gly	Phe	Tyr	Thr	Thr	Thr	Gly	Ile	Gly	Tyr	Gln	Pro	Tyr	Arg	Val					
				485					490					495						
Val	Val	Leu	Ser	Phe	Glu	Leu	Leu	Asn	Ala	Pro	Ala	Thr	Val	Cys	Gly					
			500					505					510							
Pro	Lys	Leu	Ser	Thr	Asp	Leu	Ile	Lys	Asn	Gln	Cys	Val	Asn	Phe	Asn					
		515					520					525								
Phe	Asn	Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Pro	Ser	Ser	Lys	Arg					
		530				535					540									
Phe	Gln	Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Val	Ser	Asp	Phe	Thr	Asp					
		545			550					555					560					
Ser	Val	Arg	Asp	Pro	Lys	Thr	Ser	Glu	Ile	Leu	Asp	Ile	Ser	Pro	Cys					
				565					570					575						
Ser	Phe	Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Ala	Ser	Ser					
			580					585					590							
Glu	Val	Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Asp	Val	Ser	Thr					
		595					600					605								
Ala	Ile	His	Ala	Asp	Gln	Leu	Thr	Pro	Ala	Trp	Arg	Ile	Tyr	Ser	Thr					
		610				615					620									
Gly	Asn	Asn	Val	Phe	Gln	Thr	Gln	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu					
		625			630					635					640					
His	Val	Asp	Thr	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile					
				645					650					655						
Cys	Ala	Ser	Tyr	His	Thr	Val	Ser	Leu	Leu	Arg	Ser	Thr	Ser	Gln	Lys					
			660					665					670							
Ser	Ile	Val	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Asp	Ser	Ser	Ile	Ala					
		675					680					685								
Tyr	Ser	Asn	Asn	Thr	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Ser	Ile	Ser	Ile					
		690				695					700									
Thr	Thr	Glu	Val	Met	Pro	Val	Ser	Met	Ala	Lys	Thr	Ser	Val	Asp	Cys					
					710					715					720					
Asn	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ala	Asn	Leu	Leu	Leu					
				725					730					735						
Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Ser	Gly	Ile					
			740					745					750							
Ala	Ala	Glu	Gln	Asp	Arg	Asn	Thr	Arg	Glu	Val	Phe	Ala	Gln	Val	Lys					
		755					760					765								
Gln	Met	Tyr	Lys	Thr	Pro	Thr	Leu	Lys	Tyr	Phe	Gly	Gly	Phe	Asn	Phe					
		770				775					780									
Ser	Gln	Ile	Leu	Pro	Asp	Pro	Leu	Lys	Pro	Thr	Lys	Arg	Ser	Phe	Ile					
					790					795					800					
Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly	Phe	Met					
				805					810					815						
Lys	Gln	Tyr	Gly	Glu	Cys	Leu	Gly	Asp	Ile	Asn	Ala	Arg	Asp	Leu	Ile					
			820					825						830						

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Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu	Leu	Thr	
		835					840					845				
Asp	Asp	Met	Ile	Ala	Ala	Tyr	Thr	Ala	Ala	Leu	Val	Ser	Gly	Thr	Ala	
	850					855					860					
Thr	Ala	Gly	Trp	Thr	Phe	Gly	Ala	Gly	Ala	Ala	Leu	Gln	Ile	Pro	Phe	
865					870					875					880	
Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Val	Thr	Gln	Asn	
				885					890					895		
Val	Leu	Tyr	Glu	Asn	Gln	Lys	Gln	Ile	Ala	Asn	Gln	Phe	Asn	Lys	Ala	
		900						905					910			
Ile	Ser	Gln	Ile	Gln	Glu	Ser	Leu	Thr	Thr	Thr	Ser	Thr	Ala	Leu	Gly	
		915					920					925				
Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	Ala	Gln	Ala	Leu	Asn	Thr	Leu	
	930					935					940					
Val	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	Ala	Ile	Ser	Ser	Val	Leu	Asn	
945					950					955					960	
Asp	Ile	Leu	Ser	Arg	Leu	Asp	Lys	Val	Glu	Ala	Glu	Val	Gln	Ile	Asp	
				965					970					975		
Arg	Leu	Ile	Thr	Gly	Arg	Leu	Gln	Ser	Leu	Gln	Thr	Tyr	Val	Thr	Gln	
			980				985						990			
Gln	Leu	Ile	Arg	Ala	Ala	Glu	Ile	Arg	Ala	Ser	Ala	Asn	Leu	Ala	Ala	
		995					1000					1005				
Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	Gln	Ser	Lys	Arg	Val	Asp		
	1010					1015					1020					
Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro	Gln	Ala	Ala		
	1025					1030					1035					
Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro	Ser	Gln		
	1040					1045					1050					
Glu	Arg	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Glu	Gly	Lys		
	1055					1060					1065					
Ala	Tyr	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Phe	Asn	Gly	Thr	Ser		
	1070					1075					1080					
Trp	Phe	Ile	Thr	Gln	Arg	Asn	Phe	Phe	Ser	Pro	Gln	Ile	Ile	Thr		
	1085					1090					1095					
Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	Ile	Gly		
	1100					1105					1110					
Ile	Ile	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	Leu	Asp		
	1115					1120					1125					
Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His	Thr	Ser		
	1130					1135					1140					
Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala	Ser	Val		
	1145					1150					1155					
Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val	Ala	Lys		
	1160					1165					1170					
Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly	Lys	Tyr		
	1175					1180					1185					
Glu	Gln	Tyr	Ile	Lys	Trp	Pro	Trp	Tyr	Val	Trp	Leu	Gly	Phe	Ile		
	1190					1195					1200					
Ala	Gly	Leu	Ile	Ala	Ile	Val	Met	Val	Thr	Ile	Leu	Leu	Cys	Cys		
	1205					1210					1215					

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Met	Thr	Ser	Cys	Cys	Ser	Cys	Leu	Lys	Gly	Ala	Cys	Ser	Cys	Gly
1220						1225					1230			
Ser	Cys	Cys	Lys	Phe	Asp	Glu	Asp	Asp	Ser	Glu	Pro	Val	Leu	Lys
1235						1240					1245			
Gly	Val	Lys	Leu	His	Tyr	Thr								
1250						1255								

<210> SEQ ID NO 32
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<213> ORGANISM: SARS-CoV
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<222> LOCATION: (1)..(76)
<223> OTHER INFORMATION: E protein

<400> SEQUENCE: 32

Met	Tyr	Ser	Phe	Val	Ser	Glu	Glu	Thr	Gly	Thr	Leu	Ile	Val	Asn	Ser
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Val	Leu	Leu	Phe	Phe	Ala	Phe	Val	Val	Phe	Leu	Leu	Val	Thr	Leu	Ala
			20					25					30		
Ile	Leu	Thr	Ala	Leu	Arg	Leu	Cys	Ala	Tyr	Cys	Cys	Asn	Ile	Val	Asn
		35					40					45			
Val	Ser	Leu	Val	Lys	Pro	Thr	Val	Tyr	Val	Tyr	Ser	Arg	Val	Lys	Asn
	50					55					60				
Leu	Asn	Ser	Ser	Glu	Gly	Val	Pro	Asp	Leu	Leu	Val				
65				70					75						

<210> SEQ ID NO 33
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<222> LOCATION: (1)..(221)
<223> OTHER INFORMATION: M protein

<400> SEQUENCE: 33

Met	Ala	Asp	Asn	Gly	Thr	Ile	Thr	Val	Glu	Glu	Leu	Lys	Gln	Leu	Leu
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Glu	Gln	Trp	Asn	Leu	Val	Ile	Gly	Phe	Leu	Phe	Leu	Ala	Trp	Ile	Met
		20					25						30		
Leu	Leu	Gln	Phe	Ala	Tyr	Ser	Asn	Arg	Asn	Arg	Phe	Leu	Tyr	Ile	Ile
		35					40					45			
Lys	Leu	Val	Phe	Leu	Trp	Leu	Leu	Trp	Pro	Val	Thr	Leu	Ala	Cys	Phe
	50				55						60				
Val	Leu	Ala	Ala	Val	Tyr	Arg	Ile	Asn	Trp	Val	Thr	Gly	Gly	Ile	Ala
65				70					75					80	
Ile	Ala	Met	Ala	Cys	Ile	Val	Gly	Leu	Met	Trp	Leu	Ser	Tyr	Phe	Val
			85					90						95	
Ala	Ser	Phe	Arg	Leu	Phe	Ala	Arg	Thr	Arg	Ser	Met	Trp	Ser	Phe	Asn
		100					105						110		
Pro	Glu	Thr	Asn	Ile	Leu	Leu	Asn	Val	Pro	Leu	Arg	Gly	Thr	Ile	Val
	115						120					125			
Thr	Arg	Pro	Leu	Met	Glu	Ser	Glu	Leu	Val	Ile	Gly	Ala	Val	Ile	Ile
	130					135					140				
Arg	Gly	His	Leu	Arg	Met	Ala	Gly	His	Ser	Leu	Gly	Arg	Cys	Asp	Ile

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145					150						155				160
Lys	Asp	Leu	Pro	Lys	Glu	Ile	Thr	Val	Ala	Thr	Ser	Arg	Thr	Leu	Ser
				165					170					175	
Tyr	Tyr	Lys	Leu	Gly	Ala	Ser	Gln	Arg	Val	Gly	Thr	Asp	Ser	Gly	Phe
			180					185					190		
Ala	Ala	Tyr	Asn	Arg	Tyr	Arg	Ile	Gly	Asn	Tyr	Lys	Leu	Asn	Thr	Asp
		195					200					205			
His	Ala	Gly	Ser	Asn	Asp	Asn	Ile	Ala	Leu	Leu	Val	Gln			
	210					215					220				
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<222> LOCATION: (1)..(1273)															
<223> OTHER INFORMATION: S protein															
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Met	Phe	Val	Phe	Leu	Val	Leu	Leu	Pro	Leu	Val	Ser	Ser	Gln	Cys	Val
1				5					10					15	
Asn	Leu	Thr	Thr	Arg	Thr	Gln	Leu	Pro	Pro	Ala	Tyr	Thr	Asn	Ser	Phe
			20					25					30		
Thr	Arg	Gly	Val	Tyr	Tyr	Pro	Asp	Lys	Val	Phe	Arg	Ser	Ser	Val	Leu
		35					40					45			
His	Ser	Thr	Gln	Asp	Leu	Phe	Leu	Pro	Phe	Phe	Ser	Asn	Val	Thr	Trp
	50					55					60				
Phe	His	Ala	Ile	His	Val	Ser	Gly	Thr	Asn	Gly	Thr	Lys	Arg	Phe	Asp
65					70					75					80
Asn	Pro	Val	Leu	Pro	Phe	Asn	Asp	Gly	Val	Tyr	Phe	Ala	Ser	Thr	Glu
			85						90					95	
Lys	Ser	Asn	Ile	Ile	Arg	Gly	Trp	Ile	Phe	Gly	Thr	Thr	Leu	Asp	Ser
			100					105						110	
Lys	Thr	Gln	Ser	Leu	Leu	Ile	Val	Asn	Asn	Ala	Thr	Asn	Val	Val	Ile
		115					120					125			
Lys	Val	Cys	Glu	Phe	Gln	Phe	Cys	Asn	Asp	Pro	Phe	Leu	Gly	Val	Tyr
	130						135				140				
Tyr	His	Lys	Asn	Asn	Lys	Ser	Trp	Met	Glu	Ser	Glu	Phe	Arg	Val	Tyr
145					150					155					160
Ser	Ser	Ala	Asn	Asn	Cys	Thr	Phe	Glu	Tyr	Val	Ser	Gln	Pro	Phe	Leu
			165						170					175	
Met	Asp	Leu	Glu	Gly	Lys	Gln	Gly	Asn	Phe	Lys	Asn	Leu	Arg	Glu	Phe
		180						185					190		
Val	Phe	Lys	Asn	Ile	Asp	Gly	Tyr	Phe	Lys	Ile	Tyr	Ser	Lys	His	Thr
		195					200					205			
Pro	Ile	Asn	Leu	Val	Arg	Asp	Leu	Pro	Gln	Gly	Phe	Ser	Ala	Leu	Glu
	210					215					220				
Pro	Leu	Val	Asp	Leu	Pro	Ile	Gly	Ile	Asn	Ile	Thr	Arg	Phe	Gln	Thr
225					230					235					240
Leu	Leu	Ala	Leu	His	Arg	Ser	Tyr	Leu	Thr	Pro	Gly	Asp	Ser	Ser	Ser
			245						250					255	
Gly	Trp	Thr	Ala	Gly	Ala	Ala	Ala	Tyr	Tyr	Val	Gly	Tyr	Leu	Gln	Pro
		260						265						270	

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Arg	Thr	Phe	Leu	Leu	Lys	Tyr	Asn	Glu	Asn	Gly	Thr	Ile	Thr	Asp	Ala	
		275					280					285				
Val	Asp	Cys	Ala	Leu	Asp	Pro	Leu	Ser	Glu	Thr	Lys	Cys	Thr	Leu	Lys	
	290					295					300					
Ser	Phe	Thr	Val	Glu	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	Phe	Arg	Val	
305					310					315					320	
Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn	Leu	Cys	
				325					330					335		
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala	
			340					345					350			
Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser	Val	Leu	
		355					360					365				
Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro	
	370					375					380					
Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe	
385					390					395					400	
Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly	
				405					410					415		
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys	
			420					425					430			
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn	
		435					440					445				
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe	
	450					455					460					
Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr	Pro	Cys	
465					470					475					480	
Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser	Tyr	Gly	
				485					490					495		
Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	Val	Val	
			500					505					510			
Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys	
		515					520					525				
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn	
	530					535					540					
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu	
545					550					555					560	
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Ala	Asp	Thr	Thr	Asp	Ala	Val	
				565					570					575		
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe	
			580					585					590			
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val	
		595					600					605				
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile	
	610					615					620					
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser	
625				630						635					640	
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val	
			645					650					655			
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala	
		660						665					670			

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Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Arg	Ser	Val	Ala	
		675					680					685				
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser	
	690					695					700					
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile	
705					710					715					720	
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val	
				725					730					735		
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu	
			740					745					750			
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr	
		755					760					765				
Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln	
	770					775					780					
Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe	
785					790					795					800	
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser	
			805						810					815		
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly	
			820					825					830			
Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg	Asp	
		835					840					845				
Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu	
	850					855					860					
Leu	Thr	Asp	Glu	Met	Ile	Ala	Gln	Tyr	Thr	Ser	Ala	Leu	Leu	Ala	Gly	
865					870					875					880	
Thr	Ile	Thr	Ser	Gly	Trp	Thr	Phe	Gly	Ala	Gly	Ala	Ala	Leu	Gln	Ile	
				885					890					895		
Pro	Phe	Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Val	Thr	
			900					905					910			
Gln	Asn	Val	Leu	Tyr	Glu	Asn	Gln	Lys	Leu	Ile	Ala	Asn	Gln	Phe	Asn	
		915					920					925				
Ser	Ala	Ile	Gly	Lys	Ile	Gln	Asp	Ser	Leu	Ser	Ser	Thr	Ala	Ser	Ala	
	930					935					940					
Leu	Gly	Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	Ala	Gln	Ala	Leu	Asn	
945					950					955					960	
Thr	Leu	Val	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	Ala	Ile	Ser	Ser	Val	
				965					970					975		
Leu	Asn	Asp	Ile	Leu	Ser	Arg	Leu	Asp	Lys	Val	Glu	Ala	Glu	Val	Gln	
		980						985					990			
Ile	Asp	Arg	Leu	Ile	Thr	Gly	Arg	Leu	Gln	Ser	Leu	Gln	Thr	Tyr	Val	
		995					1000					1005				
Thr	Gln	Gln	Leu	Ile	Arg	Ala	Ala	Glu	Ile	Arg	Ala	Ser	Ala	Asn		
	1010					1015					1020					
Leu	Ala	Ala	Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	Gln	Ser	Lys		
	1025					1030					1035					
Arg	Val	Asp	Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro		
	1040					1045					1050					
Gln	Ser	Ala	Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val		
	1055					1060					1065					
Pro	Ala	Gln	Glu	Lys	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His		

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1070						1075						1080			
Asp	Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	
1085						1090						1095			
Gly	Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	
1100						1105						1110			
Ile	Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	
1115						1120						1125			
Val	Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	
1130						1135						1140			
Glu	Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	
1145						1150						1155			
His	Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	
1160						1165						1170			
Ala	Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	
1175						1180						1185			
Val	Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	
1190						1195						1200			
Gly	Lys	Tyr	Glu	Gln	Tyr	Ile	Lys	Trp	Pro	Trp	Tyr	Ile	Trp	Leu	
1205						1210						1215			
Gly	Phe	Ile	Ala	Gly	Leu	Ile	Ala	Ile	Val	Met	Val	Thr	Ile	Met	
1220						1225						1230			
Leu	Cys	Cys	Met	Thr	Ser	Cys	Cys	Ser	Cys	Leu	Lys	Gly	Cys	Cys	
1235						1240						1245			
Ser	Cys	Gly	Ser	Cys	Cys	Lys	Phe	Asp	Glu	Asp	Asp	Ser	Glu	Pro	
1250						1255						1260			
Val	Leu	Lys	Gly	Val	Lys	Leu	His	Tyr	Thr						
1265						1270									

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<210> SEQ ID NO 35
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: SARS-CoV-2
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(76)
<223> OTHER INFORMATION: E protein
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<400> SEQUENCE: 35

Met	Tyr	Ser	Phe	Val	Ser	Glu	Glu	Thr	Gly	Thr	Leu	Ile	Val	Asn	Ser
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Val	Leu	Leu	Phe	Leu	Ala	Phe	Val	Val	Phe	Leu	Leu	Val	Thr	Leu	Ala
			20					25					30		
Ile	Leu	Thr	Ala	Leu	Arg	Leu	Cys	Ala	Tyr	Cys	Cys	Asn	Ile	Val	Asn
		35					40					45			
Val	Ser	Leu	Val	Lys	Pro	Thr	Val	Tyr	Val	Tyr	Ser	Arg	Val	Lys	Asn
	50					55					60				
Leu	Asn	Ser	Ser	Glu	Gly	Val	Pro	Asp	Leu	Leu	Val				
65					70					75					

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<210> SEQ ID NO 36
<211> LENGTH: 222
<212> TYPE: PRT
<213> ORGANISM: SARS-CoV-2
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1) .. (222)
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<223> OTHER INFORMATION: M protein																	
<400> SEQUENCE: 36																	
Met	Ala	Asp	Ser	Asn	Gly	Thr	Ile	Thr	Val	Glu	Glu	Leu	Lys	Lys	Leu		
1				5					10					15			
Leu	Glu	Gln	Trp	Asn	Leu	Val	Ile	Gly	Phe	Leu	Phe	Leu	Thr	Trp	Ile		
			20					25					30				
Cys	Leu	Leu	Gln	Phe	Ala	Tyr	Ala	Asn	Arg	Asn	Arg	Phe	Leu	Tyr	Ile		
		35					40					45					
Ile	Lys	Leu	Ile	Phe	Leu	Trp	Leu	Leu	Trp	Pro	Val	Thr	Leu	Ala	Cys		
	50					55				60							
Phe	Val	Leu	Ala	Ala	Val	Tyr	Arg	Ile	Asn	Trp	Ile	Thr	Gly	Gly	Ile		
65					70				75						80		
Ala	Ile	Ala	Met	Ala	Cys	Leu	Val	Gly	Leu	Met	Trp	Leu	Ser	Tyr	Phe		
				85					90					95			
Ile	Ala	Ser	Phe	Arg	Leu	Phe	Ala	Arg	Thr	Arg	Ser	Met	Trp	Ser	Phe		
		100						105					110				
Asn	Pro	Glu	Thr	Asn	Ile	Leu	Leu	Asn	Val	Pro	Leu	His	Gly	Thr	Ile		
		115				120						125					
Leu	Thr	Arg	Pro	Leu	Leu	Glu	Ser	Glu	Leu	Val	Ile	Gly	Ala	Val	Ile		
	130					135					140						
Leu	Arg	Gly	His	Leu	Arg	Ile	Ala	Gly	His	His	Leu	Gly	Arg	Cys	Asp		
145				150					155					160			
Ile	Lys	Asp	Leu	Pro	Lys	Glu	Ile	Thr	Val	Ala	Thr	Ser	Arg	Thr	Leu		
			165						170					175			
Ser	Tyr	Tyr	Lys	Leu	Gly	Ala	Ser	Gln	Arg	Val	Ala	Gly	Asp	Ser	Gly		
		180						185					190				
Phe	Ala	Ala	Tyr	Ser	Arg	Tyr	Arg	Ile	Gly	Asn	Tyr	Lys	Leu	Asn	Thr		
	195					200					205						
Asp	His	Ser	Ser	Ser	Ser	Asp	Asn	Ile	Ala	Leu	Leu	Val	Gln				
	210					215					220						
<210> SEQ ID NO 37																	
<211> LENGTH: 223																	
<212> TYPE: PRT																	
<213> ORGANISM: SARS-CoV-2																	
<220> FEATURE:																	
<221> NAME/KEY: MISC_FEATURE																	
<222> LOCATION: (1)..(223)																	
<223> OTHER INFORMATION: RBD protein																	
<400> SEQUENCE: 37																	
Arg	Val	Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn		
1				5					10					15			
Leu	Cys	Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val		
		20						25					30				
Tyr	Ala	Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser		
	35					40						45					
Val	Leu	Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val		
	50					55				60							
Ser	Pro	Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp		
65				70					75					80			
Ser	Phe	Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln		
			85						90					95			

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Thr	Gly	Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr
			100					105					110		
Gly	Cys	Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly
		115				120					125				
Gly	Asn	Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys
	130					135					140				
Pro	Phe	Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr
145					150					155					160
Pro	Cys	Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser
				165					170					175	
Tyr	Gly	Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val
			180					185					190		
Val	Val	Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly
		195						200				205			
Pro	Lys	Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	
	210					215					220				
<210> SEQ ID NO 38															
<211> LENGTH: 1353															
<212> TYPE: PRT															
<213> ORGANISM: MERS-CoV															
<220> FEATURE:															
<221> NAME/KEY: MISC_FEATURE															
<222> LOCATION: (1)..(1353)															
<223> OTHER INFORMATION: S protein															
<400> SEQUENCE: 38															
Met	Ile	His	Ser	Val	Phe	Leu	Leu	Met	Phe	Leu	Leu	Thr	Pro	Thr	Glu
1				5					10					15	
Ser	Tyr	Val	Asp	Val	Gly	Pro	Asp	Ser	Ala	Lys	Ser	Ala	Cys	Ile	Glu
			20					25					30		
Val	Asp	Ile	Gln	Gln	Thr	Phe	Phe	Asp	Lys	Thr	Trp	Pro	Arg	Pro	Ile
		35					40					45			
Asp	Val	Ser	Lys	Ala	Asp	Gly	Ile	Ile	Tyr	Pro	Gln	Gly	Arg	Thr	Tyr
	50					55					60				
Ser	Asn	Ile	Thr	Ile	Thr	Tyr	Gln	Gly	Leu	Phe	Pro	Tyr	Gln	Gly	Asp
65				70						75					80
His	Gly	Asp	Met	Tyr	Val	Tyr	Ser	Ala	Gly	His	Ala	Thr	Gly	Thr	Thr
			85						90					95	
Pro	Gln	Lys	Leu	Phe	Val	Ala	Asn	Tyr	Ser	Gln	Asp	Val	Lys	Gln	Phe
			100					105					110		
Ala	Asn	Gly	Phe	Val	Val	Arg	Ile	Gly	Ala	Ala	Ala	Asn	Ser	Thr	Gly
		115					120					125			
Thr	Val	Ile	Ile	Ser	Pro	Ser	Thr	Ser	Ala	Ile	Ile	Arg	Lys	Ile	Tyr
	130					135						140			
Pro	Ala	Phe	Met	Leu	Gly	Ser	Ser	Val	Gly	Asn	Phe	Ser	Tyr	Gly	Lys
145				150						155					160
Met	Gly	Arg	Phe	Phe	Asn	His	Thr	Leu	Val	Leu	Leu	Pro	Asp	Gly	Cys
			165						170					175	
Gly	Thr	Leu	Leu	Arg	Ala	Phe	Tyr	Cys	Ile	Leu	Glu	Pro	Arg	Ser	Gly
		180						185					190		
Asn	Tyr	Cys	Pro	Ala	Gly	Asn	Ser	Tyr	Thr	Ser	Phe	Ala	Thr	Tyr	His
	195						200					205			
Thr	Pro	Ala	Thr	Asp	Cys	Ser	Asp	Gly	Asn	Tyr	Asn	Arg	Asn	Ala	Ser

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210				215				220							
Leu	Asn	Ser	Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Arg	Asn	Cys	Thr	Phe	Met
225					230					235					240
Tyr	Thr	Tyr	Asn	Ile	Thr	Glu	Asp	Glu	Ile	Leu	Glu	Trp	Phe	Gly	Ile
				245					250					255	
Thr	Gln	Thr	Ala	Gln	Gly	Val	His	Leu	Phe	Ser	Ser	Arg	Tyr	Val	Asp
			260					265					270		
Leu	Tyr	Gly	Gly	Asn	Met	Phe	Gln	Phe	Ala	Thr	Leu	Pro	Val	Tyr	Asp
		275					280					285			
Thr	Ile	Lys	Tyr	Tyr	Ser	Ile	Ile	Pro	His	Ser	Ile	Arg	Ser	Ile	Gln
	290					295					300				
Ser	Asp	Arg	Lys	Ala	Trp	Ala	Ala	Phe	Tyr	Val	Tyr	Lys	Leu	Gln	Pro
305					310					315					320
Leu	Thr	Phe	Leu	Leu	Asp	Phe	Ser	Val	Asp	Gly	Tyr	Ile	Arg	Arg	Ala
			325						330					335	
Ile	Asp	Cys	Gly	Phe	Asn	Asp	Leu	Ser	Gln	Leu	His	Cys	Ser	Tyr	Glu
			340					345					350		
Ser	Phe	Asp	Val	Glu	Ser	Gly	Val	Tyr	Ser	Val	Ser	Ser	Phe	Glu	Ala
		355					360					365			
Lys	Pro	Ser	Gly	Ser	Val	Val	Glu	Gln	Ala	Glu	Gly	Val	Glu	Cys	Asp
	370					375					380				
Phe	Ser	Pro	Leu	Leu	Phe	Gly	Thr	Pro	Pro	Gln	Val	Tyr	Asn	Phe	Lys
385					390					395					400
Arg	Leu	Val	Phe	Thr	Asn	Cys	Asn	Tyr	Asn	Leu	Thr	Lys	Leu	Leu	Ser
			405						410					415	
Leu	Phe	Ser	Val	Asn	Asp	Phe	Thr	Cys	Ser	Gln	Ile	Ser	Pro	Ala	Ala
			420					425					430		
Ile	Ala	Ser	Asn	Cys	Tyr	Ser	Ser	Leu	Ile	Leu	Asp	Tyr	Phe	Ser	Tyr
	435						440					445			
Pro	Leu	Ser	Met	Lys	Ser	Asp	Leu	Ser	Val	Ser	Ser	Ala	Gly	Pro	Ile
	450					455					460				
Ser	Gln	Phe	Asn	Tyr	Lys	Gln	Ser	Phe	Ser	Asn	Pro	Thr	Cys	Leu	Ile
465					470					475					480
Leu	Ala	Thr	Val	Pro	His	Asn	Leu	Thr	Thr	Ile	Thr	Lys	Pro	Leu	Lys
			485						490					495	
Tyr	Ser	Tyr	Ile	Asn	Lys	Cys	Ser	Arg	Leu	Leu	Ser	Asp	Asp	Arg	Thr
			500					505					510		
Glu	Val	Leu	Gln	Leu	Val	Asn	Ala	Asn	Gln	Tyr	Ser	Pro	Cys	Val	Ser
		515					520					525			
Ile	Val	Pro	Ser	Thr	Val	Trp	Glu	Asp	Gly	Asp	Tyr	Tyr	Arg	Lys	Gln
	530					535					540				
Leu	Ser	Pro	Leu	Glu	Gly	Gly	Gly	Trp	Leu	Val	Ala	Ser	Gly	Ser	Thr
545					550					555					560
Val	Ala	Met	Thr	Glu	Gln	Leu	Gln	Met	Gly	Phe	Gly	Ile	Thr	Val	Gln
			565						570					575	
Tyr	Gly	Thr	Asp	Thr	Asn	Ser	Val	Cys	Pro	Lys	Leu	Glu	Phe	Ala	Asn
			580					585					590		
Asp	Thr	Lys	Ile	Val	Ser	Gln	Leu	Gly	Asn	Cys	Val	Glu	Tyr	Ser	Leu
		595					600					605			
Tyr	Gly	Val	Ser	Gly	Arg	Gly	Val	Phe	Gln	Asn	Cys	Thr	Ala	Val	Gly
	610					615					620				

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Val	Pro	Gln	Gln	Arg	Phe	Val	Tyr	Asp	Ala	Tyr	Gln	Asn	Leu	Val	Gly	
625					630					635					640	
Tyr	Tyr	Ser	Asp	Asp	Gly	Asn	Tyr	Tyr	Cys	Leu	Arg	Ala	Cys	Val	Ser	
			645						650					655		
Val	Pro	Val	Ser	Val	Ile	Tyr	Asp	Lys	Glu	Thr	Lys	Thr	His	Ala	Thr	
			660					665					670			
Leu	Phe	Gly	Ser	Val	Ala	Cys	Glu	His	Ile	Ser	Ser	Thr	Met	Ser	Gln	
		675					680					685				
Tyr	Ser	Arg	Ser	Thr	Arg	Ser	Met	Leu	Lys	Arg	Arg	Asp	Ser	Thr	Tyr	
	690					695					700					
Gly	Pro	Leu	Gln	Thr	Pro	Val	Gly	Cys	Val	Leu	Gly	Leu	Val	Asn	Ser	
705					710					715					720	
Ser	Leu	Phe	Val	Glu	Asp	Cys	Lys	Leu	Pro	Leu	Gly	Gln	Ser	Leu	Cys	
				725					730					735		
Ala	Leu	Pro	Asp	Thr	Pro	Ser	Thr	Leu	Thr	Pro	Arg	Ser	Val	Arg	Ser	
			740					745					750			
Val	Pro	Gly	Glu	Met	Arg	Leu	Ala	Ser	Ile	Ala	Phe	Asn	His	Pro	Ile	
		755					760					765				
Gln	Val	Asp	Gln	Leu	Asn	Ser	Ser	Tyr	Phe	Lys	Leu	Ser	Ile	Pro	Thr	
		770				775					780					
Asn	Phe	Ser	Phe	Gly	Val	Thr	Gln	Glu	Tyr	Ile	Gln	Thr	Thr	Ile	Gln	
785					790					795					800	
Lys	Val	Thr	Val	Asp	Cys	Lys	Gln	Tyr	Val	Cys	Asn	Gly	Phe	Gln	Lys	
				805					810					815		
Cys	Glu	Gln	Leu	Leu	Arg	Glu	Tyr	Gly	Gln	Phe	Cys	Ser	Lys	Ile	Asn	
			820					825					830			
Gln	Ala	Leu	His	Gly	Ala	Asn	Leu	Arg	Gln	Asp	Asp	Ser	Val	Arg	Asn	
		835					840					845				
Leu	Phe	Glu	Ser	Val	Lys	Ser	Ser	Gln	Ser	Ser	Pro	Ile	Ile	Pro	Gly	
		850				855					860					
Phe	Gly	Gly	Asp	Phe	Asn	Leu	Thr	Leu	Leu	Glu	Pro	Val	Ser	Ile	Ser	
865					870					875					880	
Thr	Gly	Ser	Arg	Ser	Ala	Arg	Ser	Ala	Ile	Glu	Asp	Leu	Leu	Phe	Asp	
				885					890					895		
Lys	Val	Thr	Ile	Ala	Asp	Pro	Gly	Tyr	Met	Gln	Gly	Tyr	Asp	Asp	Cys	
			900					905					910			
Met	Gln	Gln	Gly	Pro	Ala	Ser	Ala	Arg	Asp	Leu	Ile	Cys	Ala	Gln	Tyr	
		915					920					925				
Val	Ala	Gly	Tyr	Lys	Val	Leu	Pro	Pro	Leu	Met	Asp	Val	Asn	Met	Glu	
		930				935					940					
Ala	Ala	Tyr	Thr	Ser	Ser	Leu	Leu	Gly	Ser	Ile	Ala	Gly	Val	Gly	Trp	
945					950					955					960	
Thr	Ala	Gly	Leu	Ser	Ser	Phe	Ala	Ala	Ile	Pro	Phe	Ala	Gln	Ser	Ile	
				965					970					975		
Phe	Tyr	Arg	Leu	Asn	Gly	Val	Gly	Ile	Thr	Gln	Gln	Val	Leu	Ser	Glu	
			980				985						990			
Asn	Gln	Lys	Leu	Ile	Ala	Asn	Lys	Phe	Asn	Gln	Ala	Leu	Gly	Ala	Met	
		995					1000					1005				
Gln	Thr	Gly	Phe	Thr	Thr	Thr	Asn	Glu	Ala	Phe	Gln	Lys	Val	Gln		
	1010					1015					1020					

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Asp	Ala	Val	Asn	Asn	Asn	Ala	Gln	Ala	Leu	Ser	Lys	Leu	Ala	Ser
1025						1030					1035			
Glu	Leu	Ser	Asn	Thr	Phe	Gly	Ala	Ile	Ser	Ala	Ser	Ile	Gly	Asp
1040						1045					1050			
Ile	Ile	Gln	Arg	Leu	Asp	Val	Leu	Glu	Gln	Asp	Ala	Gln	Ile	Asp
1055						1060					1065			
Arg	Leu	Ile	Asn	Gly	Arg	Leu	Thr	Thr	Leu	Asn	Ala	Phe	Val	Ala
1070						1075					1080			
Gln	Gln	Leu	Val	Arg	Ser	Glu	Ser	Ala	Ala	Leu	Ser	Ala	Gln	Leu
1085						1090					1095			
Ala	Lys	Asp	Lys	Val	Asn	Glu	Cys	Val	Lys	Ala	Gln	Ser	Lys	Arg
1100						1105					1110			
Ser	Gly	Phe	Cys	Gly	Gln	Gly	Thr	His	Ile	Val	Ser	Phe	Val	Val
1115						1120					1125			
Asn	Ala	Pro	Asn	Gly	Leu	Tyr	Phe	Met	His	Val	Gly	Tyr	Tyr	Pro
1130						1135					1140			
Ser	Asn	His	Ile	Glu	Val	Val	Ser	Ala	Tyr	Gly	Leu	Cys	Asp	Ser
1145						1150					1155			
Ala	Asn	Pro	Thr	Asn	Cys	Ile	Ala	Pro	Val	Asn	Gly	Tyr	Phe	Ile
1160						1165					1170			
Lys	Thr	Asn	Asn	Thr	Arg	Ile	Val	Asp	Glu	Trp	Ser	Tyr	Thr	Gly
1175						1180					1185			
Ser	Ser	Phe	Tyr	Ala	Pro	Glu	Pro	Ile	Thr	Ser	Leu	Asn	Thr	Lys
1190						1195					1200			
Tyr	Val	Ala	Pro	Gln	Val	Thr	Tyr	Gln	Asn	Ile	Ser	Thr	Asn	Leu
1205						1210					1215			
Pro	Pro	Pro	Leu	Leu	Gly	Asn	Ser	Thr	Gly	Ile	Asp	Phe	Gln	Asp
1220						1225					1230			
Glu	Leu	Asp	Glu	Phe	Phe	Lys	Asn	Val	Ser	Thr	Ser	Ile	Pro	Asn
1235						1240					1245			
Phe	Gly	Ser	Leu	Thr	Gln	Ile	Asn	Thr	Thr	Leu	Leu	Asp	Leu	Thr
1250						1255					1260			
Tyr	Glu	Met	Leu	Ser	Leu	Gln	Gln	Val	Val	Lys	Ala	Leu	Asn	Glu
1265						1270					1275			
Ser	Tyr	Ile	Asp	Leu	Lys	Glu	Leu	Gly	Asn	Tyr	Thr	Tyr	Tyr	Asn
1280						1285					1290			
Lys	Trp	Pro	Trp	Tyr	Ile	Trp	Leu	Ser	Phe	Ile	Ala	Gly	Leu	Val
1295						1300					1305			
Ala	Leu	Ala	Leu	Cys	Val	Phe	Phe	Ile	Leu	Cys	Cys	Thr	Gly	Cys
1310						1315					1320			
Gly	Thr	Asn	Cys	Met	Gly	Lys	Leu	Lys	Cys	Asn	Arg	Cys	Cys	Asp
1325						1330					1335			
Arg	Tyr	Glu	Glu	Tyr	Asp	Leu	Glu	Pro	His	Lys	Val	His	Val	His
1340						1345					1350			

<210> SEQ ID NO 39
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: MERS-CoV
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(82)
<223> OTHER INFORMATION: E protein

<400> SEQUENCE: 40

<210> SEQ ID NO 41
<211> LENGTH: 389

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<212> TYPE: PRT															
<213> ORGANISM: Hepatitis B															
<220> FEATURE:															
<221> NAME/KEY: MISC_FEATURE															
<222> LOCATION: (1)..(389)															
<223> OTHER INFORMATION: L-HBsAg															
<400> SEQUENCE: 41															
Met	Gly	Thr	Asn	Leu	Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp
1				5					10					15	
His	Gln	Leu	Asp	Pro	Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp
			20					25					30		
Asp	Phe	Asn	Pro	Ile	Lys	Asp	His	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly
		35					40					45			
Val	Gly	Ala	Phe	Gly	Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Ala	Leu
	50					55					60				
Gly	Trp	Ser	Pro	Gln	Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Lys	Val
65				70					75					80	
Pro	Pro	Pro	Ala	Ser	Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro
				85					90					95	
Ile	Ser	Pro	Pro	Leu	Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn
			100					105					110		
Ser	Thr	Thr	Phe	His	Gln	Ala	Leu	Gln	Asp	Pro	Arg	Val	Arg	Gly	Leu
		115					120					125			
Tyr	Phe	Pro	Ala	Gly	Gly	Ser	Ser	Ser	Gly	Thr	Leu	Asn	Pro	Val	Gln
	130					135					140				
Asn	Ile	Ala	Ser	His	Ile	Ser	Ser	Ile	Ser	Ser	Arg	Thr	Gly	Asp	Pro
145					150					155					160
Val	Pro	Asn	Met	Glu	Asn	Ile	Thr	Ser	Gly	Phe	Leu	Gly	Pro	Leu	Leu
				165					170					175	
Val	Leu	Gln	Ala	Gly	Phe	Phe	Ser	Leu	Thr	Lys	Ile	Leu	Thr	Ile	Pro
			180					185					190		
Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Glu	Ala
		195					200					205			
Pro	Val	Cys	His	Gly	Gln	Asn	Ser	Gln	Ser	Pro	Thr	Ser	Asn	His	Ser
	210					215					220				
Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	Leu
225					230					235					240
Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe
			245						250					255	
Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu
		260						265					270		
Ile	Pro	Gly	Thr	Thr	Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	Thr
		275					280					285			
Thr	Pro	Ala	Gln	Gly	Asn	Ser	Met	Phe	Pro	Ser	Cys	Cys	Cys	Thr	Lys
	290					295					300				
Pro	Thr	Asp	Gly	Asn	Cys	Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp	Ala
305					310					315					320
Phe	Ala	Lys	Tyr	Leu	Trp	Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp	Leu
			325						330					335	
Ser	Leu	Leu	Val	Pro	Phe	Val	Gln	Trp	Phe	Ala	Gly	Leu	Ser	Pro	Thr
		340						345					350		
Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met	Trp	Tyr	Trp	Gly	Pro	Ser	Leu

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<210> SEQ ID NO 42
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Hepatitis B
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(281)
<223> OTHER INFORMATION: M-HBsAg

<400> SEQUENCE: 42
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<210> SEQ ID NO 43

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<210> SEQ ID NO 44
<211> LENGTH: 500
<212> TYPE: PRT
<213> ORGANISM: Human papillomavirus type 6
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(500)
<223> OTHER INFORMATION: L1

<400> SEQUENCE: 44

Met Trp Arg Pro Ser Asp Ser Thr Val Tyr Val Pro Pro Pro Asn Pro
1                5                10                15

Val Ser Lys Val Val Ala Thr Asp Ala Tyr Val Thr Arg Thr Asn Ile
                20                25                30

Phe Tyr His Ala Ser Ser Ser Arg Leu Leu Ala Val Gly His Pro Tyr
                35                40                45

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Phe	Ser	Ile	Lys	Arg	Ala	Asn	Lys	Thr	Val	Val	Pro	Lys	Val	Ser	Gly
50						55					60				
Tyr	Gln	Tyr	Arg	Val	Phe	Lys	Val	Val	Leu	Pro	Asp	Pro	Asn	Lys	Phe
65					70					75					80
Ala	Leu	Pro	Asp	Ser	Ser	Leu	Phe	Asp	Pro	Thr	Thr	Gln	Arg	Leu	Val
				85					90					95	
Trp	Ala	Cys	Thr	Gly	Leu	Glu	Val	Gly	Arg	Gly	Gln	Pro	Leu	Gly	Val
			100					105					110		
Gly	Val	Ser	Gly	His	Pro	Phe	Leu	Asn	Lys	Tyr	Asp	Asp	Val	Glu	Asn
		115					120					125			
Ser	Gly	Ser	Gly	Gly	Asn	Pro	Gly	Gln	Asp	Asn	Arg	Val	Asn	Val	Gly
	130					135					140				
Met	Asp	Tyr	Lys	Gln	Thr	Gln	Leu	Cys	Met	Val	Gly	Cys	Ala	Pro	Pro
145					150					155					160
Leu	Gly	Glu	His	Trp	Gly	Lys	Gly	Lys	Gln	Cys	Thr	Asn	Thr	Pro	Val
				165					170					175	
Gln	Ala	Gly	Asp	Cys	Pro	Pro	Leu	Glu	Leu	Ile	Thr	Ser	Val	Ile	Gln
			180					185					190		
Asp	Gly	Asp	Met	Val	Asp	Thr	Gly	Phe	Gly	Ala	Met	Asn	Phe	Ala	Asp
		195					200					205			
Leu	Gln	Thr	Asn	Lys	Ser	Asp	Val	Pro	Ile	Asp	Ile	Cys	Gly	Thr	Thr
	210					215					220				
Cys	Lys	Tyr	Pro	Asp	Tyr	Leu	Gln	Met	Ala	Ala	Asp	Pro	Tyr	Gly	Asp
225					230					235					240
Arg	Leu	Phe	Phe	Phe	Leu	Arg	Lys	Glu	Gln	Met	Phe	Ala	Arg	His	Phe
				245					250					255	
Phe	Asn	Arg	Ala	Gly	Glu	Val	Gly	Glu	Pro	Val	Pro	Asp	Thr	Leu	Ile
			260					265					270		
Ile	Lys	Gly	Ser	Gly	Asn	Arg	Thr	Ser	Val	Gly	Ser	Ser	Ile	Tyr	Val
	275						280					285			
Asn	Thr	Pro	Ser	Gly	Ser	Leu	Val	Ser	Ser	Glu	Ala	Gln	Leu	Phe	Asn
	290					295					300				
Lys	Pro	Tyr	Trp	Leu	Gln	Lys	Ala	Gln	Gly	His	Asn	Asn	Gly	Ile	Cys
305					310					315					320
Trp	Gly	Asn	Gln	Leu	Phe	Val	Thr	Val	Val	Asp	Thr	Thr	Arg	Ser	Thr
			325						330					335	
Asn	Met	Thr	Leu	Cys	Ala	Ser	Val	Ala	Thr	Ser	Ser	Thr	Tyr	Thr	Asn
			340					345					350		
Ser	Asp	Tyr	Lys	Glu	Tyr	Met	Arg	His	Val	Glu	Glu	Tyr	Asp	Leu	Gln
		355					360					365			
Phe	Ile	Phe	Gln	Leu	Cys	Ser	Ile	Thr	Leu	Ser	Ala	Glu	Val	Met	Ala
	370					375					380				
Tyr	Ile	His	Thr	Met	Asn	Pro	Ser	Val	Leu	Glu	Asp	Trp	Asn	Phe	Gly
385					390					395					400
Leu	Ser	Pro	Pro	Pro	Asn	Gly	Thr	Leu	Glu	Asp	Thr	Tyr	Arg	Tyr	Val
			405						410					415	
Gln	Ser	Gln	Ala	Ile	Thr	Cys	Gln	Lys	Pro	Thr	Pro	Glu	Lys	Glu	Lys
			420					425					430		
Pro	Asp	Pro	Tyr	Lys	Asn	Leu	Ser	Phe	Trp	Glu	Val	Asn	Leu	Lys	Glu
		435					440					445			
Lys	Phe	Ser	Ser	Glu	Leu	Asp	Gln	Tyr	Pro	Leu	Gly	Arg	Lys	Phe	Leu

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450				455				460							
Leu	Gln	Ser	Gly	Tyr	Arg	Gly	Arg	Ser	Ser	Ile	Arg	Thr	Gly	Val	Lys
465					470					475					480
Arg	Pro	Ala	Val	Ser	Lys	Ala	Ser	Ala	Ala	Pro	Lys	Arg	Lys	Arg	Ala
				485					490					495	
Lys	Thr	Lys	Arg												
			500												
<210> SEQ ID NO 45															
<211> LENGTH: 501															
<212> TYPE: PRT															
<213> ORGANISM: Human papillomavirus type 11															
<220> FEATURE:															
<221> NAME/KEY: MISC_FEATURE															
<222> LOCATION: (1)..(501)															
<223> OTHER INFORMATION: L1															
<400> SEQUENCE: 45															
Met	Trp	Arg	Pro	Ser	Asp	Ser	Thr	Val	Tyr	Val	Pro	Pro	Pro	Asn	Pro
1				5					10					15	
Val	Ser	Lys	Val	Val	Ala	Thr	Asp	Ala	Tyr	Val	Lys	Arg	Thr	Asn	Ile
			20					25					30		
Phe	Tyr	His	Ala	Ser	Ser	Ser	Arg	Leu	Leu	Ala	Val	Gly	His	Pro	Tyr
		35					40					45			
Tyr	Ser	Ile	Lys	Lys	Val	Asn	Lys	Thr	Val	Val	Pro	Lys	Val	Ser	Gly
	50					55					60				
Tyr	Gln	Tyr	Arg	Val	Phe	Lys	Val	Val	Leu	Pro	Asp	Pro	Asn	Lys	Phe
65					70					75					80
Ala	Leu	Pro	Asp	Ser	Ser	Leu	Phe	Asp	Pro	Thr	Thr	Gln	Arg	Leu	Val
				85					90					95	
Trp	Ala	Cys	Thr	Gly	Leu	Glu	Val	Gly	Arg	Gly	Gln	Pro	Leu	Gly	Val
			100					105						110	
Gly	Val	Ser	Gly	His	Pro	Leu	Leu	Asn	Lys	Tyr	Asp	Asp	Val	Glu	Asn
		115					120					125			
Ser	Gly	Gly	Tyr	Gly	Gly	Asn	Pro	Gly	Gln	Asp	Asn	Arg	Val	Asn	Val
	130					135					140				
Gly	Met	Asp	Tyr	Lys	Gln	Thr	Gln	Leu	Cys	Met	Val	Gly	Cys	Ala	Pro
145					150					155					160
Pro	Leu	Gly	Glu	His	Trp	Gly	Lys	Gly	Thr	Gln	Cys	Ser	Asn	Thr	Ser
				165					170					175	
Val	Gln	Asn	Gly	Asp	Cys	Pro	Pro	Leu	Glu	Leu	Ile	Thr	Ser	Val	Ile
			180					185					190		
Gln	Asp	Gly	Asp	Met	Val	Asp	Thr	Gly	Phe	Gly	Ala	Met	Asn	Phe	Ala
		195					200					205			
Asp	Leu	Gln	Thr	Asn	Lys	Ser	Asp	Val	Pro	Leu	Asp	Ile	Cys	Gly	Thr
	210					215					220				
Val	Cys	Lys	Tyr	Pro	Asp	Tyr	Leu	Gln	Met	Ala	Ala	Asp	Pro	Tyr	Gly
225					230					235					240
Asp	Arg	Leu	Phe	Phe	Tyr	Leu	Arg	Lys	Glu	Gln	Met	Phe	Ala	Arg	His
				245					250					255	
Phe	Phe	Asn	Arg	Ala	Gly	Thr	Val	Gly	Glu	Pro	Val	Pro	Asp	Asp	Leu
			260					265					270		
Leu	Val	Lys	Gly	Gly	Asn	Asn	Arg	Ser	Ser	Val	Ala	Ser	Ser	Ile	Tyr
		275					280					285			

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Val	His	Thr	Pro	Ser	Gly	Ser	Leu	Val	Ser	Ser	Glu	Ala	Gln	Leu	Phe	
	290					295					300					
Asn	Lys	Pro	Tyr	Trp	Leu	Gln	Lys	Ala	Gln	Gly	His	Asn	Asn	Gly	Ile	
305					310					315					320	
Cys	Trp	Gly	Asn	His	Leu	Phe	Val	Thr	Val	Val	Asp	Thr	Thr	Arg	Ser	
			325						330					335		
Thr	Asn	Met	Thr	Leu	Cys	Ala	Ser	Val	Ser	Lys	Ser	Ala	Thr	Tyr	Thr	
			340					345					350			
Asn	Ser	Asp	Tyr	Lys	Glu	Tyr	Met	Arg	His	Val	Glu	Glu	Phe	Asp	Leu	
		355					360					365				
Gln	Phe	Ile	Phe	Gln	Leu	Cys	Ser	Ile	Thr	Leu	Ser	Ala	Glu	Val	Met	
	370					375					380					
Ala	Tyr	Ile	His	Thr	Met	Asn	Pro	Ser	Val	Leu	Glu	Asp	Trp	Asn	Phe	
385					390					395					400	
Gly	Leu	Ser	Pro	Pro	Pro	Asn	Gly	Thr	Leu	Glu	Asp	Thr	Tyr	Arg	Tyr	
			405						410					415		
Val	Gln	Ser	Gln	Ala	Ile	Thr	Cys	Gln	Lys	Pro	Thr	Pro	Glu	Lys	Glu	
			420					425					430			
Lys	Gln	Asp	Pro	Tyr	Lys	Asp	Met	Ser	Phe	Trp	Glu	Val	Asn	Leu	Lys	
		435					440					445				
Glu	Lys	Phe	Ser	Ser	Glu	Leu	Asp	Gln	Phe	Pro	Leu	Gly	Arg	Lys	Phe	
	450					455					460					
Leu	Leu	Gln	Ser	Gly	Tyr	Arg	Gly	Arg	Thr	Ser	Ala	Arg	Thr	Gly	Ile	
465					470					475					480	
Lys	Arg	Pro	Ala	Val	Ser	Lys	Pro	Ser	Thr	Ala	Pro	Lys	Arg	Lys	Arg	
			485						490					495		
Thr	Lys	Thr	Lys	Lys												
			500													
<210> SEQ ID NO 46																
<211> LENGTH: 505																
<212> TYPE: PRT																
<213> ORGANISM: Human papillomavirus type 16																
<220> FEATURE:																
<221> NAME/KEY: MISC_FEATURE																
<222> LOCATION: (1)..(505)																
<223> OTHER INFORMATION: L1																
<400> SEQUENCE: 46																
Met	Ser	Leu	Trp	Leu	Pro	Ser	Glu	Ala	Thr	Val	Tyr	Leu	Pro	Pro	Val	
1				5					10					15		
Pro	Val	Ser	Lys	Val	Val	Ser	Thr	Asp	Glu	Tyr	Val	Ala	Arg	Thr	Asn	
			20					25					30			
Ile	Tyr	Tyr	His	Ala	Gly	Thr	Ser	Arg	Leu	Leu	Ala	Val	Gly	His	Pro	
	35					40						45				
Tyr	Phe	Pro	Ile	Lys	Lys	Pro	Asn	Asn	Asn	Lys	Ile	Leu	Val	Pro	Lys	
	50					55					60					
Val	Ser	Gly	Leu	Gln	Tyr	Arg	Val	Phe	Arg	Ile	His	Leu	Pro	Asp	Pro	
65				70					75					80		
Asn	Lys	Phe	Gly	Phe	Pro	Asp	Thr	Ser	Phe	Tyr	Asn	Pro	Asp	Thr	Gln	
			85						90					95		
Arg	Leu	Val	Trp	Ala	Cys	Val	Gly	Val	Glu	Val	Gly	Arg	Gly	Gln	Pro	
			100					105					110			

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Leu	Gly	Val	Gly	Ile	Ser	Gly	His	Pro	Leu	Leu	Asn	Lys	Leu	Asp	Asp	
		115					120					125				
Thr	Glu	Asn	Ala	Ser	Ala	Tyr	Ala	Ala	Asn	Ala	Gly	Val	Asp	Asn	Arg	
	130					135					140					
Glu	Cys	Ile	Ser	Met	Asp	Tyr	Lys	Gln	Thr	Gln	Leu	Cys	Leu	Ile	Gly	
145					150					155					160	
Cys	Lys	Pro	Pro	Ile	Gly	Glu	His	Trp	Gly	Lys	Gly	Ser	Pro	Cys	Thr	
				165					170					175		
Asn	Val	Ala	Val	Asn	Pro	Gly	Asp	Cys	Pro	Pro	Leu	Glu	Leu	Ile	Asn	
			180					185					190			
Thr	Val	Ile	Gln	Asp	Gly	Asp	Met	Val	Asp	Thr	Gly	Phe	Gly	Ala	Met	
	195						200					205				
Asp	Phe	Thr	Thr	Leu	Gln	Ala	Asn	Lys	Ser	Glu	Val	Pro	Leu	Asp	Ile	
	210					215					220					
Cys	Thr	Ser	Ile	Cys	Lys	Tyr	Pro	Asp	Tyr	Ile	Lys	Met	Val	Ser	Glu	
225					230					235					240	
Pro	Tyr	Gly	Asp	Ser	Leu	Phe	Phe	Tyr	Leu	Arg	Arg	Glu	Gln	Met	Phe	
				245					250					255		
Val	Arg	His	Leu	Phe	Asn	Arg	Ala	Gly	Ala	Val	Gly	Glu	Asn	Val	Pro	
			260					265					270			
Asp	Asp	Leu	Tyr	Ile	Lys	Gly	Ser	Gly	Ser	Thr	Ala	Asn	Leu	Ala	Ser	
		275					280					285				
Ser	Asn	Tyr	Phe	Pro	Thr	Pro	Ser	Gly	Ser	Met	Val	Thr	Ser	Asp	Ala	
	290					295					300					
Gln	Ile	Phe	Asn	Lys	Pro	Tyr	Trp	Leu	Gln	Arg	Ala	Gln	Gly	His	Asn	
305					310					315					320	
Asn	Gly	Ile	Cys	Trp	Gly	Asn	Gln	Leu	Phe	Val	Thr	Val	Val	Asp	Thr	
				325					330					335		
Thr	Arg	Ser	Thr	Asn	Met	Ser	Leu	Cys	Ala	Ala	Ile	Ser	Thr	Ser	Glu	
			340					345						350		
Thr	Thr	Tyr	Lys	Asn	Thr	Asn	Phe	Lys	Glu	Tyr	Leu	Arg	His	Gly	Glu	
		355					360					365				
Glu	Tyr	Asp	Leu	Gln	Phe	Ile	Phe	Gln	Leu	Cys	Lys	Ile	Thr	Leu	Thr	
	370					375					380					
Ala	Asp	Val	Met	Thr	Tyr	Ile	His	Ser	Met	Asn	Ser	Thr	Ile	Leu	Glu	
385						390				395					400	
Asp	Trp	Asn	Phe	Gly	Leu	Gln	Pro	Pro	Pro	Gly	Gly	Thr	Leu	Glu	Asp	
				405					410					415		
Thr	Tyr	Arg	Phe	Val	Thr	Ser	Gln	Ala	Ile	Ala	Cys	Gln	Lys	His	Thr	
			420					425					430			
Pro	Pro	Ala	Pro	Lys	Glu	Asp	Pro	Leu	Lys	Lys	Tyr	Thr	Phe	Trp	Glu	
		435					440					445				
Val	Asn	Leu	Lys	Glu	Lys	Phe	Ser	Ala	Asp	Leu	Asp	Gln	Phe	Pro	Leu	
	450					455					460					
Gly	Arg	Lys	Phe	Leu	Leu	Gln	Ala	Gly	Leu	Lys	Ala	Lys	Pro	Lys	Phe	
465					470					475					480	
Thr	Leu	Gly	Lys	Arg	Lys	Ala	Thr	Pro	Thr	Thr	Ser	Ser	Thr	Ser	Thr	
				485					490					495		
Thr	Ala	Lys	Arg	Lys	Lys	Arg	Lys	Leu								
			500					505								

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<210> SEQ ID NO 47															
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<212> TYPE: PRT															
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<223> OTHER INFORMATION: L1															
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1				5					10				15		
Leu	Tyr	Gly	Pro	Leu	Tyr	His	Pro	Gln	Pro	Leu	Pro	Leu	His	Asn	Ile
			20					25				30			
Leu	Val	Tyr	Met	Val	His	Ile	Ile	Ile	Cys	Gly	His	Tyr	Ile	Ile	Leu
		35					40					45			
Phe	Leu	Arg	Asn	Val	Asn	Val	Phe	Pro	Ile	Phe	Leu	Gln	Met	Ala	Leu
	50					55					60				
Trp	Arg	Pro	Ser	Asp	Asn	Thr	Val	Tyr	Leu	Pro	Pro	Pro	Ser	Val	Ala
65				70					75					80	
Arg	Val	Val	Asn	Thr	Asp	Asp	Tyr	Val	Thr	Arg	Thr	Ser	Ile	Phe	Tyr
			85						90				95		
His	Ala	Gly	Ser	Ser	Arg	Leu	Leu	Thr	Val	Gly	Asn	Pro	Tyr	Phe	Arg
			100					105					110		
Val	Pro	Ala	Gly	Gly	Gly	Asn	Lys	Gln	Asp	Ile	Pro	Lys	Val	Ser	Ala
		115					120					125			
Tyr	Gln	Tyr	Arg	Val	Phe	Arg	Val	Gln	Leu	Pro	Asp	Pro	Asn	Lys	Phe
	130					135					140				
Gly	Leu	Pro	Asp	Asn	Ser	Ile	Tyr	Asn	Pro	Glu	Thr	Gln	Arg	Leu	Val
145					150					155				160	
Trp	Ala	Cys	Ala	Gly	Val	Glu	Ile	Gly	Arg	Gly	Gln	Pro	Leu	Gly	Val
			165						170					175	
Gly	Leu	Ser	Gly	His	Pro	Phe	Tyr	Asn	Lys	Leu	Asp	Asp	Thr	Glu	Ser
		180						185					190		
Ser	His	Ala	Ala	Thr	Ser	Asn	Val	Ser	Glu	Asp	Val	Arg	Asp	Asn	Val
		195					200					205			
Ser	Val	Asp	Tyr	Lys	Gln	Thr	Gln	Leu	Cys	Ile	Leu	Gly	Cys	Ala	Pro
	210					215					220				
Ala	Ile	Gly	Glu	His	Trp	Ala	Lys	Gly	Thr	Ala	Cys	Lys	Ser	Arg	Pro
225					230					235				240	
Leu	Ser	Gln	Gly	Asp	Cys	Pro	Pro	Leu	Glu	Leu	Lys	Asn	Thr	Val	Leu
			245						250				255		
Glu	Asp	Gly	Asp	Met	Val	Asp	Thr	Gly	Tyr	Gly	Ala	Met	Asp	Phe	Ser
		260						265					270		
Thr	Leu	Gln	Asp	Thr	Lys	Cys	Glu	Val	Pro	Leu	Asp	Ile	Cys	Gln	Ser
		275					280					285			
Ile	Cys	Lys	Tyr	Pro	Asp	Tyr	Leu	Gln	Met	Ser	Ala	Asp	Pro	Tyr	Gly
	290					295					300				
Asp	Ser	Met	Phe	Phe	Cys	Leu	Arg	Arg	Glu	Gln	Leu	Phe	Ala	Arg	His
305					310					315				320	
Phe	Trp	Asn	Arg	Ala	Gly	Thr	Met	Gly	Asp	Thr	Val	Pro	Gln	Ser	Leu
			325						330				335		
Tyr	Ile	Lys	Gly	Thr	Gly	Met	Arg	Ala	Ser	Pro	Gly	Ser	Cys	Val	Tyr
		340						345					350		

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Ser	Pro	Ser	Pro	Ser	Gly	Ser	Ile	Val	Thr	Ser	Asp	Ser	Gln	Leu	Phe	
	355						360					365				
Asn	Lys	Pro	Tyr	Trp	Leu	His	Lys	Ala	Gln	Gly	His	Asn	Asn	Gly	Val	
	370					375					380					
Cys	Trp	His	Asn	Gln	Leu	Phe	Val	Thr	Val	Val	Asp	Thr	Thr	Arg	Ser	
385					390					395					400	
Thr	Asn	Leu	Thr	Ile	Cys	Ala	Ser	Thr	Gln	Ser	Pro	Val	Pro	Gly	Gln	
				405					410					415		
Tyr	Asp	Ala	Thr	Lys	Phe	Lys	Gln	Tyr	Ser	Arg	His	Val	Glu	Glu	Tyr	
		420						425					430			
Asp	Leu	Gln	Phe	Ile	Phe	Gln	Leu	Cys	Thr	Ile	Thr	Leu	Thr	Ala	Asp	
	435						440					445				
Val	Met	Ser	Tyr	Ile	His	Ser	Met	Asn	Ser	Ser	Ile	Leu	Glu	Asp	Trp	
	450					455					460					
Asn	Phe	Gly	Val	Pro	Pro	Pro	Pro	Thr	Thr	Ser	Leu	Val	Asp	Thr	Tyr	
465					470					475					480	
Arg	Phe	Val	Gln	Ser	Val	Ala	Ile	Thr	Cys	Gln	Lys	Asp	Ala	Ala	Pro	
				485					490					495		
Ala	Glu	Asn	Lys	Asp	Pro	Tyr	Asp	Lys	Leu	Lys	Phe	Trp	Asn	Val	Asp	
		500						505					510			
Leu	Lys	Glu	Lys	Phe	Ser	Leu	Asp	Leu	Asp	Gln	Tyr	Pro	Leu	Gly	Arg	
	515						520					525				
Lys	Phe	Leu	Val	Gln	Ala	Gly	Leu	Arg	Arg	Lys	Pro	Thr	Ile	Gly	Pro	
	530					535					540					
Arg	Lys	Arg	Ser	Ala	Pro	Ser	Ala	Thr	Thr	Ser	Ser	Lys	Pro	Ala	Lys	
545					550					555					560	
Arg	Val	Arg	Val	Arg	Ala	Arg	Lys									
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<223> OTHER INFORMATION: VP1																
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Lys	Ala	Val	Tyr	Gln	Gln	Phe	Val	Glu	Phe	Tyr	Glu	Lys	Leu	Thr	Gly	
		20						25					30			
Thr	Asp	Leu	Glu	Leu	Ile	Gln	Ile	Leu	Lys	Asp	His	Tyr	Asn	Ile	Ser	
	35					40						45				
Leu	Asp	Asn	Pro	Leu	Glu	Asn	Pro	Ser	Ser	Leu	Phe	Asp	Leu	Val	Ala	
	50					55					60					
Arg	Ile	Lys	Asn	Asn	Leu	Lys	Asn	Ser	Pro	Asp	Leu	Tyr	Ser	His	His	
65				70					75					80		
Phe	Gln	Ser	His	Gly	Gln	Leu	Ser	Asp	His	Pro	His	Ala	Leu	Ser	Ser	
		85						90					95			
Ser	Asn	Ser	His	Ala	Glu	Pro	Arg	Gly	Glu	Asn	Ala	Val	Leu	Ser	Ser	
	100						105						110			

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Glu	Asp	Leu	His	Lys	Pro	Gly	Gln	Val	Ser	Val	Gln	Leu	Pro	Gly	Thr
		115					120					125			
Asn	Tyr	Val	Gly	Pro	Gly	Asn	Glu	Leu	Gln	Ala	Gly	Pro	Pro	Gln	Ser
	130					135					140				
Ala	Val	Asp	Ser	Ala	Ala	Arg	Ile	His	Asp	Phe	Arg	Tyr	Ser	Gln	Leu
145					150					155					160
Ala	Lys	Leu	Gly	Ile	Asn	Pro	Tyr	Thr	His	Trp	Thr	Val	Ala	Asp	Glu
				165					170					175	
Glu	Leu	Leu	Glu	Asn	Ile	Lys	Asn	Glu	Thr	Gly	Phe	Gln	Ala	Gln	Val
			180					185					190		
Val	Lys	Asp	Tyr	Phe	Thr	Leu	Lys	Gly	Ala	Ala	Ala	Pro	Val	Ala	His
	195						200					205			
Phe	Gln	Gly	Ser	Leu	Pro	Glu	Val	Pro	Ala	Tyr	Asn	Ala	Ser	Glu	Lys
	210					215					220				
Tyr	Pro	Ser	Met	Thr	Ser	Val	Asn	Ser	Ala	Glu	Ala	Ser	Thr	Gly	Ala
225					230					235					240
Gly	Gly	Gly	Gly	Ser	Asn	Ser	Val	Lys	Ser	Met	Trp	Ser	Glu	Gly	Ala
				245					250					255	
Thr	Phe	Ser	Ala	Asn	Ser	Val	Thr	Cys	Thr	Phe	Ser	Arg	Gln	Phe	Leu
			260					265					270		
Ile	Pro	Tyr	Asp	Pro	Glu	His	His	Tyr	Lys	Val	Phe	Ser	Pro	Ala	Ala
		275					280					285			
Ser	Ser	Cys	His	Asn	Ala	Ser	Gly	Lys	Glu	Ala	Lys	Val	Cys	Thr	Ile
	290					295					300				
Ser	Pro	Ile	Met	Gly	Tyr	Ser	Thr	Pro	Trp	Arg	Tyr	Leu	Asp	Phe	Asn
305					310					315					320
Ala	Leu	Asn	Leu	Phe	Phe	Ser	Pro	Leu	Glu	Phe	Gln	His	Leu	Ile	Glu
				325					330					335	
Asn	Tyr	Gly	Ser	Ile	Ala	Pro	Asp	Ala	Leu	Thr	Val	Thr	Ile	Ser	Glu
		340						345					350		
Ile	Ala	Val	Lys	Asp	Val	Thr	Asp	Lys	Thr	Gly	Gly	Gly	Val	Gln	Val
	355						360					365			
Thr	Asp	Ser	Thr	Thr	Gly	Arg	Leu	Cys	Met	Leu	Val	Asp	His	Glu	Tyr
	370					375					380				
Lys	Tyr	Pro	Tyr	Val	Leu	Gly	Gln	Gly	Gln	Asp	Thr	Leu	Ala	Pro	Glu
385					390					395					400
Leu	Pro	Ile	Trp	Val	Tyr	Phe	Pro	Pro	Gln	Tyr	Ala	Tyr	Leu	Thr	Val
			405						410					415	
Gly	Asp	Val	Asn	Thr	Gln	Gly	Ile	Ser	Gly	Asp	Ser	Lys	Lys	Leu	Ala
		420						425					430		
Ser	Glu	Glu	Ser	Ala	Phe	Tyr	Val	Leu	Glu	His	Ser	Ser	Phe	Gln	Leu
		435					440					445			
Leu	Gly	Thr	Gly	Gly	Thr	Ala	Thr	Met	Ser	Tyr	Lys	Phe	Pro	Pro	Val
	450					455					460				
Pro	Pro	Glu	Asn	Leu	Glu	Gly	Cys	Ser	Gln	His	Phe	Tyr	Glu	Met	Tyr
465					470					475					480
Asn	Pro	Leu	Tyr	Gly	Ser	Arg	Leu	Gly	Val	Pro	Asp	Thr	Leu	Gly	Gly
			485						490					495	
Asp	Pro	Lys	Phe	Arg	Ser	Leu	Thr	His	Glu	Asp	His	Ala	Ile	Gln	Pro
		500						505					510		
Gln	Asn	Phe	Met	Pro	Gly	Pro	Leu	Val	Asn	Ser	Val	Ser	Thr	Lys	Glu

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515					520					525						
Gly	Asp	Ser	Ser	Ser	Thr	Gly	Ala	Gly	Lys	Ala	Leu	Thr	Gly	Leu	Ser	
530					535					540						
Thr	Gly	Thr	Ser	Gln	Asn	Thr	Arg	Ile	Ser	Leu	Arg	Pro	Gly	Pro	Val	
545					550					555					560	
Ser	Gln	Pro	Tyr	His	His	Trp	Asp	Thr	Asp	Lys	Tyr	Val	Thr	Gly	Ile	
565					570					575						
Asn	Ala	Ile	Ser	His	Gly	Gln	Thr	Thr	Tyr	Gly	Asn	Ala	Glu	Asp	Lys	
580					585					590						
Glu	Tyr	Gln	Gln	Gly	Val	Gly	Arg	Phe	Pro	Asn	Glu	Lys	Glu	Gln	Leu	
595					600					605						
Lys	Gln	Leu	Gln	Gly	Leu	Asn	Met	His	Thr	Tyr	Phe	Pro	Asn	Lys	Gly	
610					615					620						
Thr	Gln	Gln	Tyr	Thr	Asp	Gln	Ile	Glu	Arg	Pro	Leu	Met	Val	Gly	Ser	
625					630					635					640	
Val	Trp	Asn	Arg	Arg	Ala	Leu	His	Tyr	Glu	Ser	Gln	Leu	Trp	Ser	Lys	
645					650					655						
Ile	Pro	Asn	Leu	Asp	Asp	Ser	Phe	Lys	Thr	Gln	Phe	Ala	Ala	Leu	Gly	
660					665					670						
Gly	Trp	Gly	Leu	His	Gln	Pro	Pro	Pro	Gln	Ile	Phe	Leu	Lys	Ile	Leu	
675					680					685						
Pro	Pro	Ser	Gly	Pro	Ile	Gly	Gly	Ile	Lys	Ser	Met	Gly	Ile	Thr	Thr	
690					695					700						
Leu	Val	Gln	Tyr	Ala	Val	Gly	Ile	Met	Thr	Val	Thr	Met	Thr	Phe	Lys	
705					710					715					720	
Leu	Gly	Pro	Arg	Lys	Ala	Thr	Gly	Arg	Trp	Asn	Pro	Gln	Pro	Gly	Val	
725					730					735						
Tyr	Pro	Pro	His	Ala	Ala	Gly	His	Leu	Pro	Tyr	Val	Leu	Tyr	Asp	Pro	
740					745					750						
Thr	Ala	Thr	Asp	Ala	Lys	Gln	His	His	Arg	His	Gly	Tyr	Glu	Lys	Pro	
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Glu	Glu	Leu	Trp	Thr	Ala	Lys	Ser	Arg	Val	His	Pro	Leu				
770					775					780						
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20					25					30						
Ala	Asn	Ser	Val	Thr	Cys	Thr	Phe	Ser	Arg	Gln	Phe	Leu	Ile	Pro	Tyr	
35					40					45						
Asp	Pro	Glu	His	His	Tyr	Lys	Val	Phe	Ser	Pro	Ala	Ala	Ser	Ser	Cys	
50					55					60						
His	Asn	Ala	Ser	Gly	Lys	Glu	Ala	Lys	Val	Cys	Thr	Ile	Ser	Pro	Ile	
65					70					75					80	

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Met	Gly	Tyr	Ser	Thr	Pro	Trp	Arg	Tyr	Leu	Asp	Phe	Asn	Ala	Leu	Asn	
				85					90					95		
Leu	Phe	Phe	Ser	Pro	Leu	Glu	Phe	Gln	His	Leu	Ile	Glu	Asn	Tyr	Gly	
			100					105					110			
Ser	Ile	Ala	Pro	Asp	Ala	Leu	Thr	Val	Thr	Ile	Ser	Glu	Ile	Ala	Val	
		115					120					125				
Lys	Asp	Val	Thr	Asp	Lys	Thr	Gly	Gly	Gly	Val	Gln	Val	Thr	Asp	Ser	
	130					135					140					
Ser	Thr	Gly	Arg	Leu	Cys	Met	Leu	Val	Asp	His	Glu	Tyr	Lys	Tyr	Pro	
145					150				155						160	
Tyr	Val	Leu	Gly	Gln	Gly	Gln	Asp	Thr	Leu	Ala	Pro	Glu	Leu	Pro	Ile	
				165					170					175		
Trp	Val	Tyr	Phe	Pro	Pro	Gln	Tyr	Ala	Tyr	Leu	Ser	Val	Gly	Asp	Val	
			180					185					190			
Asn	Thr	Gln	Gly	Ile	Thr	Gly	Asp	Ser	Lys	Lys	Leu	Ala	Ser	Glu	Glu	
		195					200					205				
Ser	Ala	Phe	Tyr	Val	Leu	Glu	His	Ser	Ser	Phe	Gln	Leu	Leu	Gly	Thr	
	210					215					220					
Gly	Gly	Ser	Ala	Ser	Met	Ser	Tyr	Lys	Phe	Pro	Ala	Val	Pro	Pro	Glu	
225					230					235					240	
Asn	Leu	Glu	Gly	Cys	Ser	Gln	His	Phe	Tyr	Glu	Met	Tyr	Asn	Pro	Leu	
				245					250					255		
Tyr	Gly	Ser	Arg	Leu	Gly	Val	Pro	Asp	Thr	Leu	Gly	Gly	Asp	Pro	Lys	
			260					265					270			
Phe	Arg	Ser	Leu	Thr	His	Glu	Asp	His	Ala	Ile	Gln	Pro	Gln	Asn	Phe	
		275					280					285				
Met	Pro	Arg	Pro	Leu	Val	Asn	Ser	Val	Ser	Thr	Asn	Glu	Gly	Asp	Ser	
	290					295					300					
Ser	Asn	Thr	Gly	Ala	Gly	Lys	Ala	Leu	Thr	Gly	Leu	Arg	Lys	Gly	Thr	
305					310					315					320	
Ser	Gln	Asn	Thr	Arg	Ile	Ser	Leu	Arg	Pro	Gly	Pro	Val	Ser	Gln	Pro	
				325					330					335		
Tyr	His	His	Trp	Asp	Thr	Asp	Lys	Tyr	Val	Thr	Gly	Ile	Asn	Ala	Ile	
			340					345					350			
Ser	His	Gly	Gln	Thr	Thr	Tyr	Gly	Asn	Ala	Glu	Asp	Lys	Glu	Tyr	Gln	
		355					360					365				
Gln	Gly	Val	Gly	Arg	Phe	Pro	Asn	Glu	Lys	Glu	Gln	Leu	Lys	Gln	Leu	
	370					375					380					
Gln	Gly	Leu	Asn	Met	His	Thr	Tyr	Phe	Pro	Asn	Lys	Gly	Thr	Gln	Gln	
385					390					395					400	
Tyr	Thr	Asp	Gln	Ile	Glu	Arg	Pro	Leu	Met	Val	Gly	Ser	Val	Trp	Asn	
				405					410					415		
Arg	Arg	Ala	Leu	His	Tyr	Glu	Ser	Gln	Leu	Trp	Ser	Lys	Ile	Pro	Asn	
			420					425					430			
Leu	Asp	Asp	Ser	Phe	Lys	Thr	Gln	Phe	Ala	Ala	Leu	Gly	Gly	Trp	Gly	
		435					440					445				
Leu	His	Gln	Pro	Pro	Pro	Gln	Ile	Phe	Leu	Lys	Ile	Leu	Pro	Gln	Ser	
	450					455					460					
Gly	Pro	Ile	Gly	Gly	Ile	Lys	Ser	Met	Gly	Ile	Thr	Thr	Leu	Val	Gln	
465					470					475					480	

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Tyr	Ala	Val	Gly	Ile	Met	Thr	Val	Thr	Met	Thr	Ile	Lys	Leu	Gly	Pro	
				485					490					495		
Arg	Lys	Ala	Thr	Gly	Arg	Trp	Asn	Pro	Gln	Pro	Gly	Val	Tyr	Pro	Pro	
			500					505					510			
His	Ala	Ala	Gly	His	Leu	Pro	Tyr	Gly	Leu	Tyr	Asp	Pro	Thr	Ala	Thr	
			515				520					525				
Asp	Ala	Lys	Gln	His	His	Arg	His	Gly	Tyr	Glu	Lys	Pro	Glu	Glu	Leu	
	530					535					540					
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1				5					10					15		
Ala	Ser	Val	Gln	Leu	Val	Pro	Glu	Val	Asn	Ala	Ser	Asp	Pro	Leu	Ala	
			20					25					30			
Met	Asp	Pro	Val	Ala	Gly	Ser	Ser	Thr	Ala	Val	Ala	Thr	Ala	Gly	Gln	
		35					40					45				
Val	Asn	Pro	Ile	Asp	Pro	Trp	Ile	Ile	Asn	Asn	Phe	Val	Gln	Ala	Pro	
	50					55					60					
Gln	Gly	Glu	Phe	Thr	Ile	Ser	Pro	Asn	Asn	Thr	Pro	Gly	Asp	Val	Leu	
65					70					75					80	
Phe	Asp	Leu	Ser	Leu	Gly	Pro	His	Leu	Asn	Pro	Phe	Leu	Leu	His	Leu	
				85					90					95		
Ser	Gln	Met	Tyr	Asn	Gly	Trp	Val	Gly	Asn	Met	Arg	Val	Arg	Ile	Met	
			100					105					110			
Leu	Ala	Gly	Asn	Ala	Phe	Thr	Ala	Gly	Lys	Ile	Ile	Val	Ser	Cys	Ile	
		115					120					125				
Pro	Pro	Gly	Phe	Gly	Ser	Gln	Gln	Leu	Thr	Ile	Ala	Gln	Ala	Thr	Leu	
		130					135					140				
Phe	Pro	His	Val	Ile	Ala	Asp	Val	Arg	Thr	Leu	Asp	Pro	Ile	Glu	Val	
145					150					155					160	
Pro	Leu	Glu	Asp	Val	Arg	Asn	Val	Leu	Phe	His	Asn	Asn	Asp	Arg	Asn	
				165					170					175		
Gln	Gln	Thr	Met	Arg	Leu	Val	Cys	Met	Leu	Tyr	Thr	Pro	Leu	Ser	Thr	
			180					185						190		
Gly	Gly	Gly	Thr	Gly	Asp	Ser	Phe	Val	Val	Ala	Gly	Arg	Val	Met	Thr	
		195					200					205				
Cys	Pro	Ser	Pro	Asp	Phe	Asn	Phe	Leu	Phe	Leu	Val	Pro	Pro	Thr	Val	
			210				215					220				
Glu	Gln	Lys	Thr	Arg	Pro	Phe	Thr	Leu	Pro	Asn	Leu	Pro	Leu	Ser	Ser	
225						230					235				240	
Leu	Ser	Asn	Ser	Arg	Ala	Pro	Leu	Pro	Ile	Ser	Gly	Met	Gly	Ile	Ser	
				245					250					255		
Pro	Asp	Asn	Val	Gln	Ser	Val	Gln	Phe	Gln	Asn	Gly	Arg	Cys	Thr	Leu	

-continued

260					265					270						
Asp	Gly	Arg	Leu	Val	Gly	Thr	Thr	Pro	Val	Ser	Leu	Ser	His	Val	Ala	
275					280					285						
Lys	Ile	Arg	Gly	Thr	Ser	Asn	Gly	Thr	Val	Ile	Asn	Leu	Thr	Glu	Leu	
290					295					300						
Asp	Gly	Thr	Pro	Phe	His	Pro	Phe	Glu	Gly	Pro	Ala	Pro	Ile	Gly	Phe	
305					310					315					320	
Pro	Asp	Leu	Gly	Gly	Cys	Asp	Trp	His	Ile	Asn	Met	Thr	Gln	Phe	Gly	
					325					330					335	
His	Ser	Ser	Gln	Thr	Gln	Tyr	Asp	Val	Asp	Thr	Thr	Pro	Asp	Thr	Ser	
					340					345					350	
Val	Pro	His	Leu	Gly	Ser	Ile	Gln	Ala	Asn	Gly	Ile	Gly	Ser	Gly	Asn	
					355					360					365	
Tyr	Ile	Gly	Val	Leu	Ser	Trp	Val	Ser	Pro	Pro	Ser	His	Pro	Ser	Gly	
					370					375					380	
Ser	Gln	Val	Asp	Leu	Trp	Lys	Ile	Pro	Asn	Tyr	Gly	Ser	Ser	Ile	Thr	
385					390					395					400	
Glu	Ala	Thr	His	Leu	Ala	Pro	Ser	Val	Tyr	Ser	Pro	Gly	Phe	Gly	Glu	
					405					410					415	
Val	Leu	Val	Phe	Phe	Met	Ser	Lys	Ile	Pro	Gly	Pro	Gly	Gly	Asp	Ser	
					420					425					430	
Leu	Pro	Cys	Leu	Leu	Pro	Gln	Gly	Tyr	Ile	Ser	His	Leu	Ala	Ser	Glu	
					435					440					445	
Gln	Ala	Pro	Thr	Val	Gly	Glu	Gly	Pro	Leu	Leu	His	Tyr	Val	Asp	Pro	
450					455					460						
Asp	Thr	Asp	Arg	Asn	Leu	Gly	Glu	Phe	Lys	Ala	Tyr	Pro	Asp	Gly	Phe	
465					470					475					480	
Leu	Thr	Cys	Val	Pro	Asn	Gly	Ala	Ser	Ser	Gly	Pro	Gln	Gln	Leu	Pro	
					485					490					495	
Ile	Asn	Gly	Val	Phe	Val	Phe	Val	Ser	Trp	Val	Ser	Arg	Phe	Tyr	Gln	
					500					505					510	
Leu	Lys	Pro	Val	Gly	Thr	Ala	Ser	Thr	Ala	Arg	Gly	Arg	Leu	Gly	Leu	
					515					520					525	
Arg	Arg															
530																

1. An engineered cell comprising a heterologous polynucleotide encoding a viral antigen, wherein the cell is a muscle cell, a muscle precursor cell, a fibroblast, or an adipocyte from a non-human mammal, an insect, a fish, or a bird.

2. The engineered cell of claim 1, wherein the viral antigen is an influenza antigen, a coronavirus antigen, a hepatitis B antigen, a human papilloma virus antigen, a parvovirus antigen, or a Norwalk virus antigen.

3. The engineered cell of claim 2, wherein the viral antigen comprises at least a portion of a protein selected from: an influenza hemagglutinin protein, an influenza neuraminidase protein, an influenza matrix protein, a coronavirus spike protein, a coronavirus envelope protein, a coronavirus membrane protein, a coronavirus receptor binding domain protein, a major hepatitis B surface antigen protein, a human papillomavirus L1 protein, a parvovirus viral protein, and a Norwalk virus capsid protein.
4. The engineered cell of claim 1, wherein the viral antigen has a sequence that is at least 90% identical to an amino acid sequence selected from SEQ ID NOs:1-50.

5. The engineered cell of claim 3, wherein the viral antigen comprises at least a portion of an influenza hemagglutinin protein from H₁N₁, H₃N₂, or H₅N₁.

6. The engineered cell of claim 1, wherein the cell comprising one or more heterologous polynucleotides encoding an influenza hemagglutinin protein, wherein the hemagglutinin protein is selected from the group consisting of H₁N₁, H₃N₂, and H₅N₁.

7. The engineered cell of claim 1, wherein the cell is a Pax7+ mammalian muscle precursor cell.

8. The engineered cell of claim 7, wherein the cell is a Pax7+ bovine satellite cell.

9. The engineered cell of claim 1, wherein the cell is a mammalian multinucleated myotube expressing myosin heavy chain (MHC) and actin.

10. The engineered cell of claim **1**, wherein the cell is an insect muscle cell or insect muscle precursor cell.

11. The engineered cell of claim **10**, wherein the insect muscle cell is a multinucleated myotube derived from a *Drosophila* adult muscle progenitor cell (DrAMPC) or a *Manduca sexta* embryonic precursor cell (Ms-EPC).

12. The engineered cell of claim **11**, wherein the multinucleated myotube expresses myosin heavy chain and ecdysone receptor.

13. A cultured meat product comprising the engineered cell of claim **1** seeded on a food safe substrate.

14. The cultured meat product of claim **13**, wherein the substrate is a film.

15. The cultured meat product of claim **13**, wherein the substrate is a sponge or three-dimensional matrix.

16. The cultured meat product of claim **13**, wherein the substrate is a chitosan substrate.

17. The cultured meat product of claim **13**, wherein the product comprises a confluent culture of the engineered cells.

18. An edible vaccine comprising the cultured meat product comprising a heterologous polynucleotide encoding

a viral antigen, wherein the cell is a muscle cell, a muscle precursor cell, a fibroblast, or an adipocyte from a non-human mammal, an insect, a fish, or a bird.

19. An edible vaccine comprising the engineered cell comprising a heterologous polynucleotide encoding a viral antigen, wherein the cell is a muscle cell, a muscle precursor cell, a fibroblast, or an adipocyte from a non-human mammal, an insect, a fish, or a bird.

20. A method for inducing an immune response against a virus in a subject comprising administering an effective amount of the edible vaccine to the subject, the edible vaccine comprising a heterologous polynucleotide encoding a viral antigen, wherein the cell is a muscle cell, a muscle precursor cell, a fibroblast, or an adipocyte from a non-human mammal, an insect, a fish, or a bird.

21. The method of claim **20**, wherein the subject is a human.

22. The method of claim **20**, further comprising administering the edible vaccine.

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